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OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 13:01:28 ; Search time 3582 Seconds
(without alignments)
16064.488 Million cell updates/sec

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Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4683	100.0	4683	8	US-10-696-282-19	Sequence 19, Appl
3	4683	100.0	4683	8	US-10-696-900-19	Sequence 19, Appl
4	4663.8	99.6	4683	8	US-10-427-129-6	Sequence 6, Appli
5	4663.8	99.6	4683	10	US-10-959-017-2	Sequence 2, Appli
6	4663.8	99.6	4683	15	US-11-145-035-25	Sequence 25, Appl
7	4253.2	90.8	4718	7	US-10-291-583-6	Sequence 6, Appli
8	4253.2	90.8	4718	8	US-10-696-261-1	Sequence 1, Appli
9	4253.2	90.8	4718	8	US-10-696-282-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1
US-10-696-261-19
; Sequence 19, Application US/10696261
; Publication No. US20040057931A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; APPLICANT: Xiao, Weidong
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
; TITLE OF INVENTION: Vectors and Host Cells Containing Same
; FILE REFERENCE: GNVPN.031USA
; CURRENT APPLICATION NUMBER: US/10/696,261
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: US/09/807,802A
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/107,114
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 4683
; TYPE: DNA
; ORGANISM: AAV-6
US-10-696-261-19

Query Match 100.0%; Score 4683; DB 8; Length 4683;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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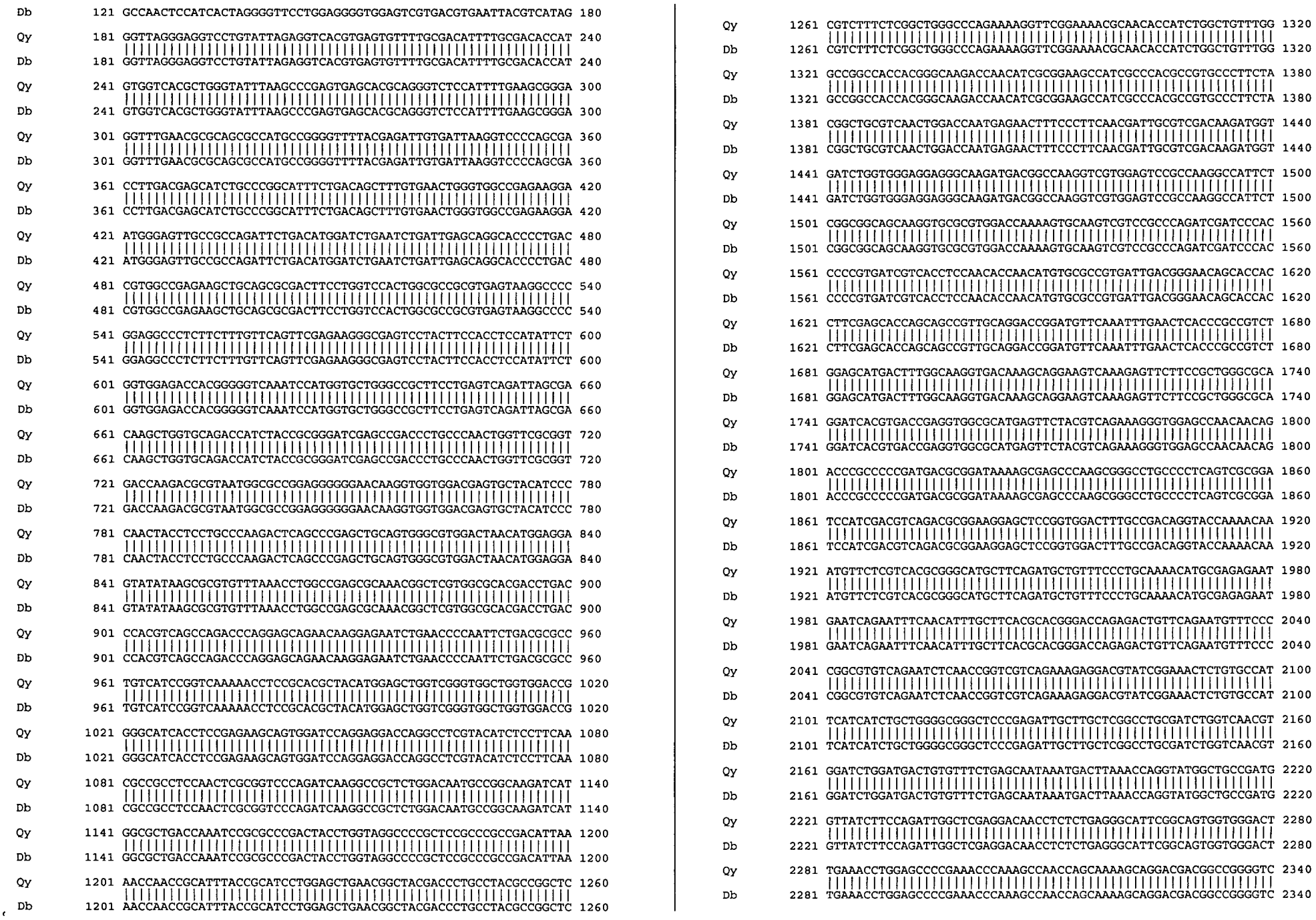
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Qy       4441 GTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCACCATA 4500
Db       4441 GTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCACCATA 4500

Qy       4501 GCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGAATACCCCTAGTGATGGAGTT 4560
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Db       4501 GCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGAATACCCCTAGTGATGGAGTT 4560

Qy       4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCG 4620

Qy       4621 TCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 TCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGC 4680

Qy       4681 CAA 4683
             |||
Db       4681 CAA 4683


RESULT 2
US-10-696-282-19
; Sequence 19, Application US/10696282
; Publication No. US20040057932A1
; GENERAL INFORMATION:
;  APPLICANT: Wilson, James M.
;  APPLICANT:  Xiao, Weidong
;  TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
;  TITLE OF INVENTION:  Vectors and Host Cells Containing Same
;  FILE REFERENCE: GNVPN.031USA
;  CURRENT APPLICATION NUMBER: US/10/696,282
;  CURRENT FILING DATE:  2003-10-29
;  PRIOR APPLICATION NUMBER: US/09/807,802A
;  PRIOR FILING DATE: 2002-02-21
;  PRIOR APPLICATION NUMBER: US 60/107,114
;  PRIOR FILING DATE: 1998-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/25694
;  PRIOR FILING DATE: 1999-11-02
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 4683
;   TYPE: DNA
;   ORGANISM: AAV-6
US-10-696-282-19

  Query Match             100.0%;  Score 4683;  DB 8;  Length 4683;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4683;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120

Qy        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180

Qy        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240

Qy        241 GTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGA 300

Qy        301 GGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGA 360

Qy        361 CCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGA 420

Qy        421 ATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGAC 480

Qy        481 CGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCGCCGCGTGAGTAAGGCCCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCGCCGCGTGAGTAAGGCCCC 540

Qy        541 GGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTACTTCCACCTCCATATTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTACTTCCACCTCCATATTCT 600

Qy        601 GGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGCGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGCGA 660

Qy        661 CAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCTGCCCAACTGGTTCGCGGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCTGCCCAACTGGTTCGCGGT 720

Qy        721 GACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCCC 780

Qy        781 CAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGGA 840

Qy        841 GTATATAAGCGCGTGTTTAAACCTGGCCGAGCGCAAACGGCTCGTGGCGCACGACCTGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GTATATAAGCGCGTGTTTAAACCTGGCCGAGCGCAAACGGCTCGTGGCGCACGACCTGAC 900

Qy        901 CCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGCC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGCC 960

Qy        961 TGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACCG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACCG 1020

Qy       1021 GGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCAA 1080

Qy       1081 CGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCAT 1140

Qy       1141 GGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACATTAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACATTAA 1200

Qy       1201 AACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCTC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCTC 1260

Qy       1261 CGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTTTGG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTTTGG 1320

Qy       1321 GCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCTA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCTA 1380

Qy       1381 CGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGGT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGGT 1440

Qy       1441 GATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTCT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTCT 1500

Qy       1501 CGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTCCGCCCAGATCGATCCCAC 1560
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Db      1501 CGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTCCGCCCAGATCGATCCCAC 1560
Qy      1561 CCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACAGCACCAC 1620
Db      1561 CCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACAGCACCAC 1620
Qy      1621 CTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATTTGAACTCACCCGCCGTCT 1680
Db      1621 CTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATTTGAACTCACCCGCCGTCT 1680
Qy      1681 GGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGAGTTCTTCCGCTGGGCGCA 1740
Db      1681 GGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGAGTTCTTCCGCTGGGCGCA 1740
Qy      1741 GGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAACAG 1800
Db      1741 GGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAACAG 1800
Qy      1801 ACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGA 1860
Db      1801 ACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGA 1860
Qy      1861 TCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGCCGACAGGTACCAAAACAA 1920
Db      1861 TCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGCCGACAGGTACCAAAACAA 1920
Qy      1921 ATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGAAT 1980
Db      1921 ATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGAAT 1980
Qy      1981 GAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGACTGTTCAGAATGTTTCCC 2040
Db      1981 GAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGACTGTTCAGAATGTTTCCC 2040
Qy      2041 CGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCAT 2100
Db      2041 CGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCAT 2100
Qy      2101 TCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGT 2160
Db      2101 TCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGT 2160
Qy      2161 GGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAACCAGGTATGGCTGCCGATG 2220
Db      2161 GGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAACCAGGTATGGCTGCCGATG 2220
Qy      2221 GTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGGCAGTGGTGGGACT 2280
Db      2221 GTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGGCAGTGGTGGGACT 2280
Qy      2281 TGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTC 2340
Db      2281 TGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTC 2340
Qy      2341 TGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCG 2400
Db      2341 TGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCG 2400
Qy      2401 TCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAG 2460
Db      2401 TCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAG 2460
Qy      2461 CGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGC 2520
Db      2461 CGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGC 2520
Qy      2521 AAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGAGGG 2580
Db      2521 AAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGAGGG 2580
Qy      2581 TTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCCTGGAAAGAAACGTC 2640
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Db      2581 TTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCCTGGAAAGAAACGTC 2640
Qy      2641 CGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGC 2700
Db      2641 CGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGC 2700
Qy      2701 AGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACC 2760
Db      2701 AGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACC 2760
Qy      2761 CACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTT 2820
Db      2761 CACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTT 2820
Qy      2821 CAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCT 2880
Db      2821 CAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCT 2880
Qy      2881 CAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCC 2940
Db      2881 CAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCC 2940
Qy      2941 GAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAA 3000
Db      2941 GAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAA 3000
Qy      3001 CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATT 3060
Db      3001 CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATT 3060
Qy      3061 TCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATT 3120
Db      3061 TCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATT 3120
Qy      3121 GGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCA 3180
Db      3121 GGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCA 3180
Qy      3181 CGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTGT 3240
Db      3181 CGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTGT 3240
Qy      3241 CGGACTCGGAGTACCAGTTCCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTC 3300
Db      3241 CGGACTCGGAGTACCAGTTCCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTC 3300
Qy      3301 CGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCA 3360
Db      3301 CGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCA 3360
Qy      3361 GCCAGGCAGTGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGA 3420
Db      3361 GCCAGGCAGTGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGA 3420
Qy      3421 GAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCT 3480
Db      3421 GAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCT 3480
Qy      3481 ACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATT 3540
Db      3481 ACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATT 3540
Qy      3541 ACCTGAACAGAACTCACAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCC 3600
Db      3541 ACCTGAACAGAACTCACAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCC 3600
Qy      3601 GTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACC 3660
Db      3601 GTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACC 3660
Qy      3661 GGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTG 3720
Db      3661 GGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTG 3720
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Qy       3721 GTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGG 3780

Qy       3781 CCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAA 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 CCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAA 3840

Qy       3841 AGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGG 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 AGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGG 3900

Qy       3901 AAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCC 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 AAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCC 3960

Qy       3961 AGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAA 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 AGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAA 4020

Qy       4021 TGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACA 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 TGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACA 4080

Qy       4081 CGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTC 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 CGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTC 4140

Qy       4141 CTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTA 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 CTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTA 4200

Qy       4201 CAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAAT 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 CAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAAT 4260

Qy       4261 GGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACT 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 GGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACT 4320

Qy       4321 ATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTC 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 ATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTC 4380

Qy       4381 GCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCG 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 GCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCG 4440

Qy       4441 GTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCACCATA 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 GTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCACCATA 4500

Qy       4501 GCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGAATACCCCTAGTGATGGAGTT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 GCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGAATACCCCTAGTGATGGAGTT 4560

Qy       4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCG 4620

Qy       4621 TCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 TCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGC 4680

Qy       4681 CAA 4683
             |||
Db       4681 CAA 4683


RESULT 3
US-10-696-900-19
; Sequence 19, Application US/10696900
; Publication No. US20040057933A1
; GENERAL INFORMATION:
;  APPLICANT: Wilson, James M.
;  APPLICANT:  Xiao, Weidong
;  TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
;  TITLE OF INVENTION:  Vectors and Host Cells Containing Same
;  FILE REFERENCE: GNVPN.031USA
;  CURRENT APPLICATION NUMBER: US/10/696,900
;  CURRENT FILING DATE:  2003-10-30
;  PRIOR APPLICATION NUMBER: US/09/807,802A
;  PRIOR FILING DATE: 2002-02-21
;  PRIOR APPLICATION NUMBER: US 60/107,114
;  PRIOR FILING DATE: 1998-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/25694
;  PRIOR FILING DATE: 1999-11-02
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 4683
;   TYPE: DNA
;   ORGANISM: AAV-6
US-10-696-900-19

  Query Match             100.0%;  Score 4683;  DB 8;  Length 4683;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4683;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120

Qy        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180

Qy        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240

Qy        241 GTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGA 300

Qy        301 GGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGA 360

Qy        361 CCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGA 420

Qy        421 ATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGAC 480

Qy        481 CGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCGCCGCGTGAGTAAGGCCCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCGCCGCGTGAGTAAGGCCCC 540

Qy        541 GGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTACTTCCACCTCCATATTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTACTTCCACCTCCATATTCT 600

Qy        601 GGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGCGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGCGA 660

Qy        661 CAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCTGCCCAACTGGTTCGCGGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        661 CAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCTGCCCAACTGGTTCGCGGT 720
Qy        721 GACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCCC 780
Db        721 GACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCCC 780
Qy        781 CAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGGA 840
Db        781 CAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGGA 840
Qy        841 GTATATAAGCGCGTGTTTAAACCTGGCCGAGCGCAAACGGCTCGTGGCGCACGACCTGAC 900
Db        841 GTATATAAGCGCGTGTTTAAACCTGGCCGAGCGCAAACGGCTCGTGGCGCACGACCTGAC 900
Qy        901 CCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGCC 960
Db        901 CCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGCC 960
Qy        961 TGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACCG 1020
Db        961 TGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACCG 1020
Qy       1021 GGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCAA 1080
Db       1021 GGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCAA 1080
Qy       1081 CGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCAT 1140
Db       1081 CGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCAT 1140
Qy       1141 GGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACATTAA 1200
Db       1141 GGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACATTAA 1200
Qy       1201 AACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCTC 1260
Db       1201 AACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCTC 1260
Qy       1261 CGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTTTGG 1320
Db       1261 CGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTTTGG 1320
Qy       1321 GCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCTA 1380
Db       1321 GCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCTA 1380
Qy       1381 CGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGGT 1440
Db       1381 CGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGGT 1440
Qy       1441 GATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTCT 1500
Db       1441 GATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTCT 1500
Qy       1501 CGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTCCGCCCAGATCGATCCCAC 1560
Db       1501 CGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTCCGCCCAGATCGATCCCAC 1560
Qy       1561 CCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACAGCACCAC 1620
Db       1561 CCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACAGCACCAC 1620
Qy       1621 CTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATTTGAACTCACCCGCCGTCT 1680
Db       1621 CTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATTTGAACTCACCCGCCGTCT 1680
Qy       1681 GGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGAGTTCTTCCGCTGGGCGCA 1740
Db       1681 GGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGAGTTCTTCCGCTGGGCGCA 1740
Qy       1741 GGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAACAG 1800
Db       1741 GGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAACAG 1800

Qy       1801 ACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGA 1860
Db       1801 ACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGA 1860
Qy       1861 TCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGCCGACAGGTACCAAAACAA 1920
Db       1861 TCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGCCGACAGGTACCAAAACAA 1920
Qy       1921 ATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGAAT 1980
Db       1921 ATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGAAT 1980
Qy       1981 GAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGACTGTTCAGAATGTTTCCC 2040
Db       1981 GAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGACTGTTCAGAATGTTTCCC 2040
Qy       2041 CGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCAT 2100
Db       2041 CGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCAT 2100
Qy       2101 TCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGT 2160
Db       2101 TCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGT 2160
Qy       2161 GGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAACCAGGTATGGCTGCCGATG 2220
Db       2161 GGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAACCAGGTATGGCTGCCGATG 2220
Qy       2221 GTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGGCAGTGGTGGGACT 2280
Db       2221 GTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGGCAGTGGTGGGACT 2280
Qy       2281 TGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTC 2340
Db       2281 TGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTC 2340
Qy       2341 TGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCG 2400
Db       2341 TGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCG 2400
Qy       2401 TCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAG 2460
Db       2401 TCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAG 2460
Qy       2461 CGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGC 2520
Db       2461 CGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGC 2520
Qy       2521 AAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGAGGG 2580
Db       2521 AAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGAGGG 2580
Qy       2581 TTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCCTGGAAAGAAACGTC 2640
Db       2581 TTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCCTGGAAAGAAACGTC 2640
Qy       2641 CGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGC 2700
Db       2641 CGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGC 2700
Qy       2701 AGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACC 2760
Db       2701 AGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACC 2760
Qy       2761 CACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTT 2820
Db       2761 CACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTT 2820
Qy       2821 CAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCT 2880
Db       2821 CAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCT 2880
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Qy       2881 CAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCC 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 CAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCC 2940

Qy       2941 GAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAA 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 GAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAA 3000

Qy       3001 CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATT 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATT 3060

Qy       3061 TCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATT 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATT 3120

Qy       3121 GGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCA 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCA 3180

Qy       3181 CGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTGT 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTGT 3240

Qy       3241 CGGACTCGGAGTACCAGTTCCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTC 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 CGGACTCGGAGTACCAGTTCCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTC 3300

Qy       3301 CGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCA 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 CGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCA 3360

Qy       3361 GCCAGGCAGTGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGA 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GCCAGGCAGTGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGA 3420

Qy       3421 GAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCT 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 GAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCT 3480

Qy       3481 ACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATT 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 ACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATT 3540

Qy       3541 ACCTGAACAGAACTCACAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCC 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 ACCTGAACAGAACTCACAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCC 3600

Qy       3601 GTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACC 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 GTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACC 3660

Qy       3661 GGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTG 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 GGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTG 3720

Qy       3721 GTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGG 3780

Qy       3781 CCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAA 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 CCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAA 3840

Qy       3841 AGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGG 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 AGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGG 3900

Qy       3901 AAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCC 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 AAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCC 3960

Qy       3961 AGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAA 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 AGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAA 4020

Qy       4021 TGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACA 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 TGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACA 4080

Qy       4081 CGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTC 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 CGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTC 4140

Qy       4141 CTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTA 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 CTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTA 4200

Qy       4201 CAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAAT 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 CAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAAT 4260

Qy       4261 GGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACT 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 GGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACT 4320

Qy       4321 ATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTC 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 ATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTC 4380

Qy       4381 GCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCG 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 GCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCG 4440

Qy       4441 GTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCACCATA 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 GTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCACCATA 4500

Qy       4501 GCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGAATACCCCTAGTGATGGAGTT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 GCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGAATACCCCTAGTGATGGAGTT 4560

Qy       4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCG 4620

Qy       4621 TCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 TCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGC 4680

Qy       4681 CAA 4683
             |||
Db       4681 CAA 4683
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RESULT 4
US-10-427-129-6
; Sequence 6, Application US/10427129
; Publication No. US20040101514A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Yuhong
; APPLICANT: Luo, Jia
; APPLICANT: During, Matthew
; TITLE OF INVENTION: High Transgene Expression of A Pseudotyped Adeno-Associated Virus
; FILE REFERENCE: 102182-24
; CURRENT APPLICATION NUMBER: US/10/427,129
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: 09/804,898
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/189,110
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 4683
; TYPE: DNA

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;   ORGANISM: adeno-associated virus 2
US-10-427-129-6

  Query Match             99.6%;  Score 4663.8;  DB 8;  Length 4683;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 4671;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120

Qy        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180

Qy        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240

Qy        241 GTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGA 300

Qy        301 GGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGA 360

Qy        361 CCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGA 420

Qy        421 ATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGAC 480

Qy        481 CGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCGCCGCGTGAGTAAGGCCCC 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCAGTGGCGCCGCGTGAGTAAGGCCCC 540

Qy        541 GGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTACTTCCACCTCCATATTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTACTTCCACCTCCATATTCT 600

Qy        601 GGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGCGA 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        601 GGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGGGA 660

Qy        661 CAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCTGCCCAACTGGTTCGCGGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCTGCCCAACTGGTTCGCGGT 720

Qy        721 GACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCCC 780

Qy        781 CAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGGA 840

Qy        841 GTATATAAGCGCGTGTTTAAACCTGGCCGAGCGCAAACGGCTCGTGGCGCACGACCTGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GTATATAAGCGCGTGTTTAAACCTGGCCGAGCGCAAACGGCTCGTGGCGCACGACCTGAC 900

Qy        901 CCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGCC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGCC 960

Qy        961 TGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACCG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        961 TGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACCG 1020

Qy       1021 GGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCAA 1080

Qy       1081 CGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCAT 1140

Qy       1141 GGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACATTAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACATTAA 1200

Qy       1201 AACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCTC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCTC 1260

Qy       1261 CGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTTTGG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTTTGG 1320

Qy       1321 GCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCTA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCTA 1380

Qy       1381 CGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGGT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGGT 1440

Qy       1441 GATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTCT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTCT 1500

Qy       1501 CGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTCCGCCCAGATCGATCCCAC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTCCGCCCAGATCGATCCCAC 1560

Qy       1561 CCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACAGCACCAC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACAGCACCAC 1620

Qy       1621 CTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATTTGAACTCACCCGCCGTCT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATTTGAACTCACCCGCCGTCT 1680

Qy       1681 GGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGAGTTCTTCCGCTGGGCGCA 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGAGTTCTTCCGCTGGGCGCA 1740

Qy       1741 GGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAACAG 1800
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1741 GGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAAGAG 1800

Qy       1801 ACCCGCCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 ACCCGCCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGA 1860

Qy       1861 TCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGCCGACAGGTACCAAAACAA 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGCCGACAGGTACCAAAACAA 1920

Qy       1921 ATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGAAT 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 ATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGAAT 1980

Qy       1981 GAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGACTGTTCAGAATGTTTCCC 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGACTGTTCAGAATGTTTCCC 2040

Qy       2041 CGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCAT 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCAT 2100
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Qy      2101 TCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGT 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 TCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGT 2160

Qy      2161 GGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAACCAGGTATGGCTGCCGATG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 GGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAACCAGGTATGGCTGCCGATG 2220

Qy      2221 GTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGGCAGTGGTGGGACT 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 GTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGGACT 2280

Qy      2281 TGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTC 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 TGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTC 2340

Qy      2341 TGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 TGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCG 2400

Qy      2401 TCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAG 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 TCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAG 2460

Qy      2461 CGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 CGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGC 2520

Qy      2521 AAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGAGGG 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 AAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGAGGG 2580

Qy      2581 TTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCCTGGAAAGAAACGTC 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 TTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCCTGGAAAGAAACGTC 2640

Qy      2641 CGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGC 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641 CGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGC 2700

Qy      2701 AGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACC 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 AGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACC 2760

Qy      2761 CACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTT 2820
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Db      2761 CACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTT 2820

Qy      2821 CAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCT 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821 CAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCT 2880

Qy      2881 CAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCC 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2881 CAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCC 2940

Qy      2941 GAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAA 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941 GAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAA 3000

Qy      3001 CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATT 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3001 CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATT 3060

Qy      3061 TCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATT 3120
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Db      3061 TCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATT 3120

Qy      3121 GGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCA 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3121 GGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCA 3180

Qy      3181 CGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTGT 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3181 CGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTCT 3240

Qy      3241 CGGACTCGGAGTACCAGTTCCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTC 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3241 CGGACTCGGAGTACCAGTTGCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTC 3300

Qy      3301 CGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCA 3360
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Db      3301 CGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCA 3360

Qy      3361 GCCAGGCAGTGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGA 3420
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Db      3361 GCCAGGCAGTGGGACGGTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGA 3420

Qy      3421 GAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCT 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3421 GAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCT 3480

Qy      3481 ACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATT 3540
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Db      3481 ACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATT 3540

Qy      3541 ACCTGAACAGAACTCACAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCC 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      3601 GTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACC 3660
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      3661 GGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTG 3720
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Qy      3721 GTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGG 3780
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Db      3721 GTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGG 3780

Qy      3781 CCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAA 3840
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Qy      3841 AGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGG 3900
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Db      3841 AGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGG 3900

Qy      3901 AAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCC 3960
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Qy      3961 AGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAA 4020
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Qy      4021 TGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACA 4080
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Db      4081 CGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTC 4140

Qy      4141 CTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTA 4200
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Db      4141 CTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTA 4200

Qy      4201 CAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAAT 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 CAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAAT 4260

Qy      4261 GGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACT 4320
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Db       4261 GGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACT 4320

Qy       4321 ATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTC 4380
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Db       4321 ATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTC 4380

Qy       4381 GCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCG 4440
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Db       4381 GCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCG 4440

Qy       4441 GTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCACCATA 4500
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Qy       4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCG 4620
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Db       4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCG 4620

Qy       4621 TCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGC 4680
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Db       4621 TCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGG 4680

Qy       4681 CAA 4683
             |||
Db       4681 CAA 4683


RESULT 5
US-10-959-017-2
; Sequence 2, Application US/10959017
; Publication No. US20050106125A1
; GENERAL INFORMATION:
;  APPLICANT: FALCK-PEDERSEN, ERIK S
;  APPLICANT:  PHILPOTT, NICOLA
;  TITLE OF INVENTION: USE OF AAV INTEGRATION EFFICIENCY ELEMENT FOR MEDIATING
;  TITLE OF INVENTION:  SITE-SPECIFIC INTEGRATION OF A TRANSCRIPTION UNIT
;  FILE REFERENCE: 230526
;  CURRENT APPLICATION NUMBER: US/10/959,017
;  CURRENT FILING DATE:  2004-10-05
;  PRIOR APPLICATION NUMBER: PCT/US03/11191
;  PRIOR FILING DATE: 2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/371,044
;  PRIOR FILING DATE: 2002-04-09
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 4683
;   TYPE: DNA
;   ORGANISM: adeno-associated virus serotype 6
US-10-959-017-2

  Query Match             99.6%;  Score 4663.8;  DB 10;  Length 4683;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 4671;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120

Qy        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180

Qy        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240

Qy        241 GTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGA 300

Qy        301 GGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGA 360

Qy        361 CCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGA 420

Qy        421 ATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGAC 480

Qy        481 CGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCGCCGCGTGAGTAAGGCCCC 540
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        481 CGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCAGTGGCGCCGCGTGAGTAAGGCCCC 540

Qy        541 GGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTACTTCCACCTCCATATTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTACTTCCACCTCCATATTCT 600

Qy        601 GGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGCGA 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        601 GGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGGGA 660

Qy        661 CAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCTGCCCAACTGGTTCGCGGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCTGCCCAACTGGTTCGCGGT 720

Qy        721 GACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCCC 780

Qy        781 CAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGGA 840

Qy        841 GTATATAAGCGCGTGTTTAAACCTGGCCGAGCGCAAACGGCTCGTGGCGCACGACCTGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GTATATAAGCGCGTGTTTAAACCTGGCCGAGCGCAAACGGCTCGTGGCGCACGACCTGAC 900

Qy        901 CCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGCC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGCC 960

Qy        961 TGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACCG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACCG 1020

Qy       1021 GGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCAA 1080

Qy       1081 CGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCAT 1140

Qy       1141 GGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACATTAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACATTAA 1200

Qy       1201 AACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCTC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCTC 1260

Qy       1261 CGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTTTGG 1320
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Db       1261 CGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTTTGG 1320
Qy       1321 GCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCTA 1380
Db       1321 GCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCTA 1380
Qy       1381 CGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGGT 1440
Db       1381 CGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGGT 1440
Qy       1441 GATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTCT 1500
Db       1441 GATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTCT 1500
Qy       1501 CGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTCCGCCCAGATCGATCCCAC 1560
Db       1501 CGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTCCGCCCAGATCGATCCCAC 1560
Qy       1561 CCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACAGCACCAC 1620
Db       1561 CCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACAGCACCAC 1620
Qy       1621 CTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATTTGAACTCACCCGCCGTCT 1680
Db       1621 CTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATTTGAACTCACCCGCCGTCT 1680
Qy       1681 GGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGAGTTCTTCCGCTGGGCGCA 1740
Db       1681 GGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGAGTTCTTCCGCTGGGCGCA 1740
Qy       1741 GGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAACAG 1800
Db       1741 GGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAAGAG 1800
Qy       1801 ACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGA 1860
Db       1801 ACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGA 1860
Qy       1861 TCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGCCGACAGGTACCAAAACAA 1920
Db       1861 TCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGCCGACAGGTACCAAAACAA 1920
Qy       1921 ATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGAAT 1980
Db       1921 ATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGAAT 1980
Qy       1981 GAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGACTGTTCAGAATGTTTCCC 2040
Db       1981 GAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGACTGTTCAGAATGTTTCCC 2040
Qy       2041 CGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCAT 2100
Db       2041 CGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCAT 2100
Qy       2101 TCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGT 2160
Db       2101 TCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGT 2160
Qy       2161 GGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAACCAGGTATGGCTGCCGATG 2220
Db       2161 GGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAACCAGGTATGGCTGCCGATG 2220
Qy       2221 GTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGGCAGTGGTGGGACT 2280
Db       2221 GTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGGACT 2280
Qy       2281 TGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTC 2340
Db       2281 TGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTC 2340
Qy       2341 TGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCG 2400
Db       2341 TGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCG 2400
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Qy       2401 TCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAG 2460
Db       2401 TCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAG 2460
Qy       2461 CGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGC 2520
Db       2461 CGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGC 2520
Qy       2521 AAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGAGGG 2580
Db       2521 AAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGAGGG 2580
Qy       2581 TTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCCTGGAAAGAAACGTC 2640
Db       2581 TTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCCTGGAAAGAAACGTC 2640
Qy       2641 CGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGC 2700
Db       2641 CGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGC 2700
Qy       2701 AGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACC 2760
Db       2701 AGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACC 2760
Qy       2761 CACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTT 2820
Db       2761 CACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTT 2820
Qy       2821 CAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCT 2880
Db       2821 CAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCT 2880
Qy       2881 CAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCC 2940
Db       2881 CAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCC 2940
Qy       2941 GAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAA 3000
Db       2941 GAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAA 3000
Qy       3001 CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATT 3060
Db       3001 CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATT 3060
Qy       3061 TCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATT 3120
Db       3061 TCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATT 3120
Qy       3121 GGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCA 3180
Db       3121 GGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCA 3180
Qy       3181 CGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTGT 3240
Db       3181 CGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTCT 3240
Qy       3241 CGGACTCGGAGTACCAGTTCCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTC 3300
Db       3241 CGGACTCGGAGTACCAGTTGCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTC 3300
Qy       3301 CGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCA 3360
Db       3301 CGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCA 3360
Qy       3361 GCCAGGCAGTGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGA 3420
Db       3361 GCCAGGCAGTGGGACGGTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGA 3420
Qy       3421 GAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCT 3480
Db       3421 GAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCT 3480
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Qy       3481 ACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATT 3540
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Db       3481 ACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATT 3540

Qy       3541 ACCTGAACAGAACTCACAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCC 3600
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3541 ACCTGAACAGAACTCAGAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCC 3600

Qy       3601 GTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACC 3660
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 GGGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACC 3660

Qy       3661 GGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTG 3720
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Db       3661 GGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTG 3720

Qy       3721 GTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGG 3780
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Db       3721 GTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGG 3780

Qy       3781 CCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAA 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 CCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAA 3840

Qy       3841 AGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGG 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 AGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGG 3900

Qy       3901 AAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCC 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 AAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCC 3960

Qy       3961 AGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAA 4020
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Db       3961 AGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAA 4020

Qy       4021 TGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACA 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 TGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACA 4080

Qy       4081 CGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTC 4140
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Db       4081 CGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTC 4140

Qy       4141 CTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTA 4200
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Db       4141 CTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTA 4200

Qy       4201 CAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAAT 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 CAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAAT 4260

Qy       4261 GGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACT 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 GGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACT 4320

Qy       4321 ATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTC 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 ATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTC 4380

Qy       4381 GCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCG 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 GCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCG 4440

Qy       4441 GTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCACCATA 4500
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       4441 GTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCGTTATTATCTTATCTGGTCACCATA 4500

Qy       4501 GCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGAATACCCCTAGTGATGGAGTT 4560
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Db       4501 GCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGAATACCCCTAGTGATGGAGTT 4560

Qy       4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCG 4620
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Db       4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCG 4620

Qy       4621 TCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 TCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGG 4680

Qy       4681 CAA 4683
             |||
Db       4681 CAA 4683
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RESULT 6
US-11-145-035-25
; Sequence 25, Application US/11145035
; Publication No. US20050287122A1
; GENERAL INFORMATION:
; APPLICANT: Bartlett et al.
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/41335
; CURRENT APPLICATION NUMBER: US/11/145,035
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/038,972
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 4683
; TYPE: DNA
; ORGANISM: Adeno-associate virus 6
US-11-145-035-25

Query Match 99.6%; Score 4663.8; DB 15; Length 4683;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 4671; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
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Db         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120

Qy        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180
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Db        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180

Qy        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240

Qy        241 GTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGA 300

Qy        301 GGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGA 360

Qy        361 CCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGA 420

Qy        421 ATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGAC 480

Qy        481 CGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCGCCGCGTGAGTAAGGCCCC 540
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
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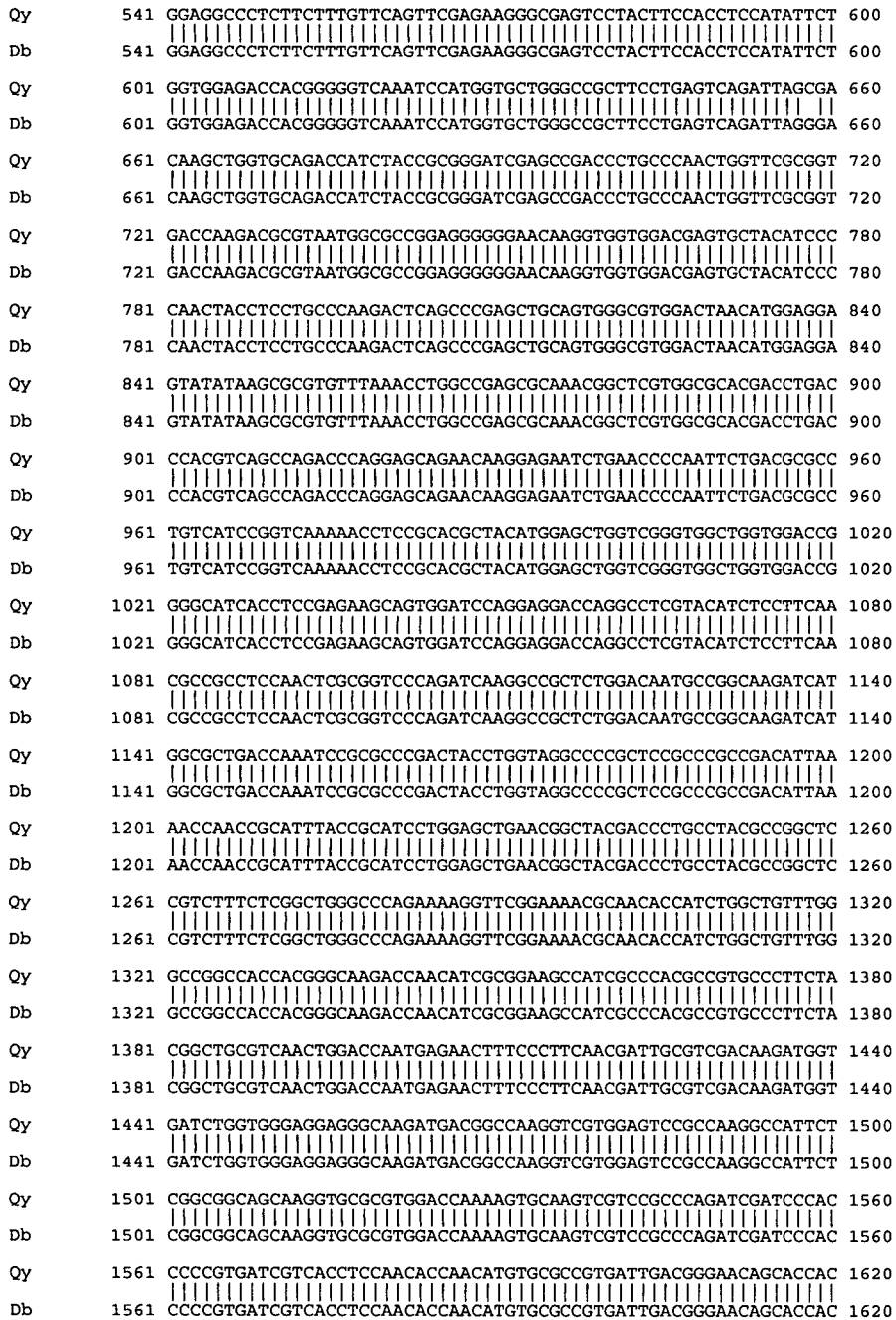
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Db 601 GGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGGGA 660
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Qy 781 CAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGGA 840
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Qy 1801 ACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGA 1860
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Qy 2041 CGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCAT 2100
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Qy       4081 CGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTC 4140
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Qy       4141 CTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTA 4200
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Db       4141 CTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTA 4200

Qy       4201 CAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAAT 4260
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Db       4201 CAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAAT 4260

Qy       4261 GGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACT 4320
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Db       4321 ATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTC 4380

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Qy       4441 GTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCACCATA 4500
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Db       4441 GTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCGTTATTATCTTATCTGGTCACCATA 4500

Qy       4501 GCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGAATACCCCTAGTGATGGAGTT 4560
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Qy       4681 CAA 4683
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Db       4681 CAA 4683
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RESULT 7
US-10-291-583-6
; Sequence 6, Application US/10291583
; Publication No. US20030138772A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Guangping
; APPLICANT: Wilson, James M.
; APPLICANT: Alvira, Mauricio
; TITLE OF INVENTION: A Method of Detecting and/or Identifying Adeno-Associated Virus (
; TITLE OF INVENTION: Sequences and Isolating No. US20030138772A1el Sequences Identifi

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;  FILE REFERENCE: UPN-02735USA
;  CURRENT APPLICATION NUMBER: US/10/291,583
;  CURRENT FILING DATE:  2002-11-12
;  PRIOR APPLICATION NUMBER: US 60/350,607
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/341,117
;  PRIOR FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: US 60/377,066
;  PRIOR FILING DATE: 2002-05-01
;  PRIOR APPLICATION NUMBER: US 60/386,675
;  PRIOR FILING DATE: 2002-06-05
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 4718
;   TYPE: DNA
;   ORGANISM: adeno-associated virus serotype 1
US-10-291-583-6

  Query Match             90.8%;  Score 4253.2;  DB 7;  Length 4718;
  Best Local Similarity   94.7%;  Pred. No. 0;
  Matches 4471;  Conservative    0;  Mismatches  208;  Indels   43;  Gaps    5;

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              |||||||||||||||| |||| ||    ||||||  || | ||||||||||  |||||
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Qy        283 CTCCATTTTGAAGCGGGAGGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGT 342
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Db        298 CTCCATTTTGACCGCGAAATTTGAACGAGCAGCAGCCATGCCGGGCTTCTACGAGATCGT 357

Qy        343 GATTAAGGTCCCCAGCGACCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAA 402
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Qy        463 TGAGCAGGCACCCCTGACCGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCG 522
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Db        838 GTGGACTAACATGGAGGAGTATATAAGCGCCTGTTTGAACCTGGCCGAGCGCAAACGGCT 897

Qy        883 CGTGGCGCACGACCTGACCCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAA 942
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 CGTGGCGCAGCACCTGACCCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAA 957

Qy        943 CCCCAATTCTGACGCGCCTGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGT 1002
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        958 CCCCAATTCTGACGCGCCTGTCATCCGGTCAAAAACCTCCGCGCGCTACATGGAGCTGGT 1017

Qy       1003 CGGGTGGCTGGTGGACCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGC 1062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 CGGGTGGCTGGTGGACCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGC 1077

Qy       1063 CTCGTACATCTCCTTCAACGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGA 1122
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1078 CTCGTACATCTCCTTCAACGCCGCTTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGA 1137

Qy       1123 CAATGCCGGCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGC 1182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 CAATGCCGGCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGC 1197

Qy       1183 TCCGCCCGCCGACATTAAAACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGA 1242
              ||||||||| |||||||||||||||||||| |||||||||||||||||||||||||||||
Db       1198 TCCGCCCGCGGACATTAAAACCAACCGCATCTACCGCATCCTGGAGCTGAACGGCTACGA 1257

Qy       1243 CCCTGCCTACGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAA 1302
              |||||||||||||||||||||||||||||||||||||||||||||||||| || |||||
Db       1258 ACCTGCCTACGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGGAAGCGCAA 1317

Qy       1303 CACCATCTGGCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGC 1362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1318 CACCATCTGGCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGC 1377

Qy       1363 CCACGCCGTGCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGA 1422
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1378 CCACGCCGTGCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAATGA 1437

Qy       1423 TTGCGTCGACAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGA 1482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1438 TTGCGTCGACAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGA 1497

Qy       1483 GTCCGCCAAGGCCATTCTCGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTC 1542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1498 GTCCGCCAAGGCCATTCTCGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTC 1557

Qy       1543 CGCCCAGATCGATCCCACCCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGAT 1602
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1558 CGCCCAGATCGACCCCACCCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGAT 1617

Qy       1603 TGACGGGAACAGCACCACCTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATT 1662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1618 TGACGGGAACAGCACCACCTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATT 1677

Qy       1663 TGAACTCACCCGCCGTCTGGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGA 1722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1678 TGAACTCACCCGCCGTCTGGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGA 1737

Qy       1723 GTTCTTCCGCTGGGCGCAGGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAA 1782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1738 GTTCTTCCGCTGGGCGCAGGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAA 1797

Qy       1783 GGGTGGAGCCAACAACAGACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGC 1842
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1798 GGGTGGAGCCAACAAAAGACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGC 1857
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Qy       1843 CTGCCCCTCAGTCGCGGATCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGC 1902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1858 CTGCCCCTCAGTCGCGGATCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGC 1917

Qy       1903 CGACAGGTACCAAAACAAATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTG 1962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1918 CGACAGGTACCAAAACAAATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTG 1977

Qy       1963 CAAAACATGCGAGAGAATGAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGA 2022
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db       1978 CAAGACATGCGAGAGAATGAATCAGAATTTCAACATTTGCTTCACGCACGGGACGAGAGA 2037

Qy       2023 CTGTTCAGAATGTTTCCCCGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTA 2082
             ||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2038 CTGTTCAGAGTGCTTCCCCGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTA 2097

Qy       2083 TCGGAAACTCTGTGCCATTCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGC 2142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2098 TCGGAAACTCTGTGCCATTCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGC 2157

Qy       2143 CTGCGATCTGGTCAACGTGGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAAC 2202
             ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       2158 CTGCGATCTGGTCAACGTGGACCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAAC 2217

Qy       2203 CAGGTATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCA 2262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2218 CAGGTATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCA 2277

Qy       2263 TTCGGCAGTGGTGGGACTTGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGC 2322
             ||||  |||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       2278 TTCGCGAGTGGTGGGACTTGAAACCTGGAGCCCCGAAGCCCAAAGCCAACCAGCAAAAGC 2337

Qy       2323 AGGACGACGGCCGGGGTCTGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGAC 2382
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2338 AGGACGACGGCCGGGGTCTGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGAC 2397

Qy       2383 TCGACAAGGGGGAGCCCGTCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCT 2442
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       2398 TCGACAAGGGGGAGCCCGTCAACGCGGCGGACGCAGCGGCCCTCGAGCACGACAAGGCCT 2457

Qy       2443 ACGACCAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCG 2502
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2458 ACGACCAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCG 2517

Qy       2503 AGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCT 2562
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2518 AGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCT 2577

Qy       2563 TCCAGGCCAAGAAGAGGGTTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGG 2622
             |||||||||||||| |||||||||||||| | |||||||||||||||| ||||||||||
Db       2578 TCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGTCTGGTTGAGGAAGGCGCTAAGACGG 2637

Qy       2623 CTCCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCA 2682
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2638 CTCCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCA 2697

Qy       2683 TTGGCAAGACAGGCCAGCAGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACT 2742
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2698 TCGGCAAGACAGGCCAGCAGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACT 2757

Qy       2743 CAGAGTCAGTCCCCGACCCACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGG 2802
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       2758 CAGAGTCAGTCCCCGATCCACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGG 2817

Qy       2803 GACCTACTACAATGGCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCG 2862
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2818 GACCTACTACAATGGCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCG 2877

Qy       2863 ACGGAGTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAG 2922
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2878 ACGGAGTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAG 2937

Qy       2923 TCATCACCACCAGCACCCGAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGC 2982
             |||||||||||||||||| || |||||||||||||||| || ||||||||||||||||||
Db       2938 TCATCACCACCAGCACCCGCACCTGGGCCTTGCCCACCTACAATAACCACCTCTACAAGC 2997

Qy       2983 AAATCTCCAGTGCTTCAACGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCC 3042
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2998 AAATCTCCAGTGCTTCAACGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCC 3057

Qy       3043 CCTGGGGGTATTTTGATTTCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGC 3102
             |||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db       3058 CCTGGGGGTATTTTGATTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGC 3117

Qy       3103 GACTCATCAACAACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACA 3162
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       3118 GACTCATCAACAACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAAACTCTTCAACA 3177

Qy       3163 TCCAAGTCAAGGAGGTCACGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCA 3222
             |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       3178 TCCAAGTCAAGGAGGTCACGACGAATGATGGCGTCACAACCATCGCTAATAACCTTACCA 3237

Qy       3223 GCACGGTTCAAGTCTTGTCGGACTCGGAGTACCAGTTCCCGTACGTCCTCGGCTCTGCGC 3282
             |||||||||||||||| |||||||||||||||||| | ||||||||||||||||||||||
Db       3238 GCACGGTTCAAGTCTTCTCGGACTCGGAGTACCAGCTTCCGTACGTCCTCGGCTCTGCGC 3297

Qy       3283 ACCAGGGCTGCCTCCCTCCGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACC 3342
             |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       3298 ACCAGGGCTGCCTCCCTCCGTTCCCGGCGGACGTGTTCATGATTCCGCAATACGGCTACC 3357

Qy       3343 TAACGCTCAACAATGGCAGCCAGGCAGTGGGACGCTCATCCTTTTACTGCCTGGAATATT 3402
             | |||||||||||||||||||| || |||||||| |||||||||||||||||||||||||
Db       3358 TGACGCTCAACAATGGCAGCCAAGCCGTGGGACGTTCATCCTTTTACTGCCTGGAATATT 3417

Qy       3403 TCCCATCGCAGATGCTGAGAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACG 3462
             |||| || |||||||||||||||||||| |||||||||||||||||||||| ||||| |
Db       3418 TCCCTTCTCAGATGCTGAGAACGGGCAACAACTTTACCTTCAGCTACACCTTTGAGGAAG 3477

Qy       3463 TGCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCA 3522
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3478 TGCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCA 3537

Qy       3523 TCGACCAGTACCTGTATTACCTGAACAGAACTCACAATCAGTCCGGAAGTGCCCAAAACA 3582
             ||||||| |||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db       3538 TCGACCAATACCTGTATTACCTGAACAGAACTCAAAATCAGTCCGGAAGTGCCCAAAACA 3597

Qy       3583 AGGACTTGCTGTTTAGCCGTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGC 3642
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3598 AGGACTTGCTGTTTAGCCGTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGC 3657

Qy       3643 TACCTGGACCCTGTTACCGGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACA 3702
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3658 TACCTGGACCCTGTTATCGGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACA 3717

Qy       3703 GCAACTTTACCTGGACTGGTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCA 3762
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Db       3718 GCAATTTTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGGCGTGAATCCATCATCA 3777

Qy       3763 ACCCTGGCACTGCTATGGCCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCG 3822
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Db       3778 ACCCTGGCACTGCTATGGCCTCACACAAAGACGACGAAGACAAGTTCTTTCCCATGAGCG 3837

Qy       3823 GTGTCATGATTTTTGGAAAGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCA 3882
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Db       3838 GTGTCATGATTTTTGGAAAAGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCA 3897

Qy       3883 TGATCACAGACGAAGAGGAAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGA 3942
             |||| |||||||||||||||| |||||||||||||| ||||||||||||||||||||||||
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Qy       3943 CTGTGGCAGTCAATCTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTA 4002
             | |||||||||||| |||||||||||||||||||||||||||||||||||||||||| ||
Db       3958 CCGTGGCAGTCAATTTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGCTA 4017

Qy       4003 TGGGAGCCTTACCTGGAATGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTT 4062
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Db       4018 TGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTT 4077

Qy       4063 GGGCCAAAATTCCTCACACGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTG 4122
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Db       4078 GGGCCAAAATTCCTCACACAGATGGACACTTTCACCCGTCTCCTCTTATGGGCGGCTTTG 4137

Qy       4123 GACTTAAGCACCCGCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTC 4182
                ||||  ||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4138 GACTCAAGAACCCGCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTC 4197

Qy       4183 CGGCAGAGTTTTCGGCTACAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAG 4242
                ||||  |||||||| |||||||||||||||||||||||||||| || ||||||||||||||
Db       4198 CGGCGGAGTTTTCAGCTACAAAGTTTGCTTCATTCATCACCCAATACTCCACAGGACAAG 4257

Qy       4243 TGAGCGTGGAGATTGAATGGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAG 4302
                ||||  ||||| |||||||||||||||||||||||||||||||| ||||||||||||||||
Db       4258 TGAGTGTGGAAATTGAATGGGAGCTGCAGAAAGAAAACAGCAAGCGCTGGAATCCCGAAG 4317

Qy       4303 TGCAGTATACATCTAACTATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATG 4362
                |||||||  |||||  || |||||||||||||||||||||||||||| ||||||||||||||||
Db       4318 TGCAGTACACATCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAATG 4377

Qy       4363 GACTTTATACTGAGCCTCGCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGT 4422
                ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       4378 GACTTTATACTGAGCCTCGCCCCATTGGCACCCGTTACCTTACCCGTCCCCTGTAATTAC 4437

Qy       4423 GTGTTAATCAATAAACCGGTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTA 4482
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Db       4438 GTGTTAATCAATAAACCGGTTGATTCGTTTCAGTTGAACTTTGGTCTCCTGTCCTTCTTA 4497

Qy       4483 TCTTATCTGGTCACCATAGCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGA-- 4540
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Db       4498 TCTTATC-GGTTACCATGGTTATAGCTTACACATTAACTGCTTGGTTGCGCTTCGCGATA 4556

Qy       4541 -------------------ATACCCCTAGTGATGGAGTTGCCCACTCCCTCTATGCGCGC 4581
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Db       4557 AAAGACTTACGTCATCGGGTTACCCCTAGTGATGGAGTTGCCCACTCCCTCTCTGCGCGC 4616

Qy       4582 TCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCGTCTGCGGACCTTTGGTCCGCA 4641
                |||||||||||||||||| || || || || || || | | || || || || || ||
Db       4617 TCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGCAGACGGCAGAGCTCTGCTCTGCC 4676

Qy       4642 GGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGCCAA 4683
                |||||||||||||||||||||||| |||||||||| |||
Db       4677 GGCCCCACCGAGCGAGCGAGCGCGCAGAGAGGGAGTGGGCAA 4718


RESULT 8
US-10-696-261-1
; Sequence 1, Application US/10696261
; Publication No. US20040057931A1
; GENERAL INFORMATION:
;  APPLICANT: Wilson, James M.
;  APPLICANT:  Xiao, Weidong
;  TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
;  TITLE OF INVENTION:  Vectors and Host Cells Containing Same
;  FILE REFERENCE: GNVPN.031USA
;  CURRENT APPLICATION NUMBER: US/10/696,261
;  CURRENT FILING DATE:  2003-10-29
;  PRIOR APPLICATION NUMBER: US/09/807,802A
;  PRIOR FILING DATE: 2002-02-21
;  PRIOR APPLICATION NUMBER: US 60/107,114
;  PRIOR FILING DATE: 1998-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/25694
;  PRIOR FILING DATE: 1999-11-02
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 4718
;   TYPE: DNA
;   ORGANISM: AAV-1
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (335)..(2206)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2223)..(4430)
;   OTHER INFORMATION:
US-10-696-261-1

  Query Match             90.8%;  Score 4253.2;  DB 8;  Length 4718;
  Best Local Similarity   94.7%;  Pred. No. 0;
  Matches 4471;  Conservative    0;  Mismatches  208;  Indels   43;  Gaps    5;

Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
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Db          1 TTGCCCACTCCCTCTCTGCGCGCTCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGC 60

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
               |||| | | ||| ||| | | ||||| ||  ||||||||||||||||||||||||||||
Db         61 AGACGGCAGAGCTCTGCTCTGCCGGCCCCACCGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120

Qy        121 GCCAACTCCATCACTAGGGGT----------------TCCTGGAGGGGTGGAGTCGTGA 163
              | |||||||||||||||||||                |    |   ||   |||
Db        121 GGCAACTCCATCACTAGGGGTAATCGCGAAGCGCCTCCCACGCTGCCGCGTCAGCGCTGA 180

Qy        164 CGTGAATTACGTCATAGGGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTG-TTTTGC 222
              ||| ||||||||||||||   | | ||||||||||||  |||||||||||| ||||||
Db        181 CGTAAATTACGTCATAGGG---GAGTGGTCCTGTATTAGCTGTCACGTGAGTGCTTTTGC 237

Qy        223 GACATTTTGCGACACCATGTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGT 282
              |||||||||||||||||| |||| ||     |||||| || | ||||||||||  ||||| |
Db        238 GACATTTTGCGACACCACGTGGCCATTTAGGGTATATATGGCCGAGTGAGCGAGCAGGAT 297

Qy        283 CTCCATTTTGAAGCGGGAGGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGT 342
              ||||||||||    | |  ||  |          ||||||||||  || ||||||| ||
Db        298 CTCCATTTTGACCGCGAAATTTGAACGAGCAGCAGCCATGCCGGGCTTCTACGAGATCGT 357

Qy        343 GATTAAGGTCCCCAGCGACCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAA 402
              ||| ||||| || |||||||| |||||||| ||||| ||||||||||||   |||||||
Db        358 GATCAAGGTGCCGAGCGACCTGGACGAGCACCTGCCGGGCATTTCTGACTCGTTTGTGAG 417

Qy        403 CTGGGTGGCCGAGAAGGAATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGAT 462
              |||||||||||||||||||||||||||||||| |||| || ||||||||||||||||||||
Db        418 CTGGGTGGCCGAGAAGGAATGGGAGCTGCCCCCGGATTCTGACATGGATCTGAATCTGAT 477

Qy        463 TGAGCAGGCACCCCTGACCGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCG 522
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Db        478 TGAGCAGGCACCCCTGACCGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCAATGGCG 537

Qy        523 CCGCGTGAGTAAGGCCCCGGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTA 582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 CCGCGTGAGTAAGGCCCCGGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTA 597

Qy        583 CTTCCACCTCCATATTCTGGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTT 642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 CTTCCACCTCCATATTCTGGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTT 657

Qy        643 CCTGAGTCAGATTAGCGACAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCT 702
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        658 CCTGAGTCAGATTAGGGACAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCT 717

Qy        703 GCCCAACTGGTTCGCGGTGACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGT 762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 GCCCAACTGGTTCGCGGTGACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGT 777

Qy        763 GGACGAGTGCTACATCCCCAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGC 822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 GGACGAGTGCTACATCCCCAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGC 837

Qy        823 GTGGACTAACATGGAGGAGTATATAAGCGCGTGTTTAAACCTGGCCGAGCGCAAACGGCT 882
              |||||||||||||||||||||||||||||| ||||| ||||||||||||||||||||||
Db        838 GTGGACTAACATGGAGGAGTATATAAGCGCCTGTTTGAACCTGGCCGAGCGCAAACGGCT 897
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Qy       883 CGTGGCGCACGACCTGACCCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAA 942
Db       898 CGTGGCGCAGCACCTGACCCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAA 957

Qy       943 CCCCAATTCTGACGCGCCTGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGT 1002
Db       958 CCCCAATTCTGACGCGCCTGTCATCCGGTCAAAAACCTCCGCGCGCTACATGGAGCTGGT 1017

Qy      1003 CGGGTGGCTGGTGGACCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGC 1062
Db      1018 CGGGTGGCTGGTGGACCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGC 1077

Qy      1063 CTCGTACATCTCCTTCAACGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGA 1122
Db      1078 CTCGTACATCTCCTTCAACGCCGCTTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGA 1137

Qy      1123 CAATGCCGGCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGC 1182
Db      1138 CAATGCCGGCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGC 1197

Qy      1183 TCCGCCCGCCGACATTAAAACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGA 1242
Db      1198 TCCGCCCGCGGACATTAAAACCAACCGCATCTACCGCATCCTGGAGCTGAACGGCTACGA 1257

Qy      1243 CCCTGCCTACGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAA 1302
Db      1258 ACCTGCCTACGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGGAAGCGCAA 1317

Qy      1303 CACCATCTGGCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGC 1362
Db      1318 CACCATCTGGCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGC 1377

Qy      1363 CCACGCCGTGCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGA 1422
Db      1378 CCACGCCGTGCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAATGA 1437

Qy      1423 TTGCGTCGACAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGA 1482
Db      1438 TTGCGTCGACAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGA 1497

Qy      1483 GTCCGCCAAGGCCATTCTCGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTC 1542
Db      1498 GTCCGCCAAGGCCATTCTCGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTC 1557

Qy      1543 CGCCCAGATCGATCCCACCCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGAT 1602
Db      1558 CGCCCAGATCGACCCCACCCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGAT 1617

Qy      1603 TGACGGGAACAGCACCACCTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATT 1662
Db      1618 TGACGGGAACAGCACCACCTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATT 1677

Qy      1663 TGAACTCACCCGCCGTCTGGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGA 1722
Db      1678 TGAACTCACCCGCCGTCTGGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGA 1737

Qy      1723 GTTCTTCCGCTGGGCGCAGGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAA 1782
Db      1738 GTTCTTCCGCTGGGCGCAGGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAA 1797

Qy      1783 GGGTGGAGCCAACAACAGACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGC 1842
Db      1798 GGGTGGAGCCAACAAAAGACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGC 1857

Qy      1843 CTGCCCCTCAGTCGCGGATCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGC 1902
Db      1858 CTGCCCCTCAGTCGCGGATCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGC 1917

Qy      1903 CGACAGGTACCAAAACAAATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTG 1962
Db      1918 CGACAGGTACCAAAACAAATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTG 1977

Qy      1963 CAAAACATGCGAGAGAATGAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGA 2022
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Db      1978 CAAGACATGCGAGAGAATGAATCAGAATTTCAACATTTGCTTCACGCACGGGACGAGAGA 2037

Qy      2023 CTGTTCAGAATGTTTCCCCGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTA 2082
Db      2038 CTGTTCAGAGTGCTTCCCCGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTA 2097

Qy      2083 TCGGAAACTCTGTGCCATTCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGC 2142
Db      2098 TCGGAAACTCTGTGCCATTCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGC 2157

Qy      2143 CTGCGATCTGGTCAACGTGGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAAC 2202
Db      2158 CTGCGATCTGGTCAACGTGGACCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAAC 2217

Qy      2203 CAGGTATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCA 2262
Db      2218 CAGGTATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCA 2277

Qy      2263 TTCGGCAGTGGTGGGACTTGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGC 2322
Db      2278 TTCGCGAGTGGTGGGACTTGAAACCTGGAGCCCCGAAGCCCAAAGCCAACCAGCAAAAGC 2337

Qy      2323 AGGACGACGGCCGGGGTCTGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGAC 2382
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Qy      2383 TCGACAAGGGGGAGCCCGTCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCT 2442
Db      2398 TCGACAAGGGGGAGCCCGTCAACGCGGCGGACGCAGCGGCCCTCGAGCACGACAAGGCCT 2457

Qy      2443 ACGACCAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCG 2502
Db      2458 ACGACCAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCG 2517

Qy      2503 AGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCT 2562
Db      2518 AGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCT 2577

Qy      2563 TCCAGGCCAAGAAGAGGGTTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGG 2622
Db      2578 TCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGTCTGGTTGAGGAAGGCGCTAAGACGG 2637

Qy      2623 CTCCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCA 2682
Db      2638 CTCCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCA 2697

Qy      2683 TTGGCAAGACAGGCCAGCAGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACT 2742
Db      2698 TCGGCAAGACAGGCCAGCAGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACT 2757

Qy      2743 CAGAGTCAGTCCCCGACCCACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGG 2802
Db      2758 CAGAGTCAGTCCCCGATCCACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGG 2817

Qy      2803 GACCTACTACAATGGCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCG 2862
Db      2818 GACCTACTACAATGGCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCG 2877

Qy      2863 ACGGAGTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAG 2922
Db      2878 ACGGAGTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAG 2937

Qy      2923 TCATCACCACCAGCACCCGAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGC 2982
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Db      2998 AAATCTCCAGTGCTTCAACGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCC 3057

Qy      3043 CCTGGGGGTATTTTGATTTCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGC 3102
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Db       3058 CCTGGGGGTATTTTGATTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGC 3117

Qy       3103 GACTCATCAACAACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACA 3162

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Qy       3463 TGCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCA 3522

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Qy       3523 TCGACCAGTACCTGTATTACCTGAACAGAACTCACAATCAGTCCGGAAGTGCCCAAAACA 3582

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Db       3598 AGGACTTGCTGTTTAGCCGTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGC 3657

Qy       3643 TACCTGGACCCTGTTACCGGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACA 3702

Db       3658 TACCTGGACCCTGTTATCGGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACA 3717

Qy       3703 GCAACTTTACCTGGACTGGTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCA 3762

Db       3718 GCAATTTTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGGCGTGAATCCATCATCA 3777

Qy       3763 ACCCTGGCACTGCTATGGCCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCG 3822

Db       3778 ACCCTGGCACTGCTATGGCCTCACACAAAGACGACGAAGACAAGTTCTTTCCCATGAGCG 3837

Qy       3823 GTGTCATGATTTTTGGAAAGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCA 3882

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Qy       3883 TGATCACAGACGAAGAGGAAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGA 3942

Db       3898 TGATTACAGACGAAGAGGAAATTAAAGCCACTAACCCTGTGGCCACCGAAAGATTTGGGA 3957

Qy       3943 CTGTGGCAGTCAATCTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTA 4002

Db       3958 CCGTGGCAGTCAATTTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGCTA 4017

Qy       4003 TGGGAGCCTTACCTGGAATGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTT 4062

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Qy       4123 GACTTAAGCACCCGCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTC 4182

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Qy       4183 CGGCAGAGTTTTCGGCTACAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAG 4242

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Qy       4243 TGAGCGTGGAGATTGAATGGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAG 4302

Db       4258 TGAGTGTGGAAATTGAATGGGAGCTGCAGAAAGAAAACAGCAAGCGCTGGAATCCCGAAG 4317

Qy       4303 TGCAGTATACATCTAACTATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATG 4362

Db       4318 TGCAGTACACATCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAATG 4377

Qy       4363 GACTTTATACTGAGCCTCGCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGT 4422

Db       4378 GACTTTATACTGAGCCTCGCCCCATTGGCACCCGTTACCTTACCCGTCCCCTGTAATTAC 4437

Qy       4423 GTGTTAATCAATAAACCGGTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTA 4482

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Qy       4582 TCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCGTCTGCGGACCTTTGGTCCGCA 4641

Db       4617 TCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGCAGACGGCAGAGCTCTGCTCTGCC 4676

Qy       4642 GGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGCCAA 4683

Db       4677 GGCCCCACCGAGCGAGCGAGCGCGCAGAGAGGGAGTGGGCAA 4718
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RESULT 9
US-10-696-282-1
; Sequence 1, Application US/10696282
; Publication No. US20040057932A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; APPLICANT: Xiao, Weidong
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
; TITLE OF INVENTION: Vectors and Host Cells Containing Same
; FILE REFERENCE: GNVPN.031USA
; CURRENT APPLICATION NUMBER: US/10/696,282
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: US/09/807,802A
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/107,114
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4718
; TYPE: DNA
; ORGANISM: AAV-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (335)..(2206)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2223)..(4430)
; OTHER INFORMATION:
US-10-696-282-1

Query Match 90.8%; Score 4253.2; DB 8; Length 4718;

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  Best Local Similarity   94.7%;  Pred. No. 0;
  Matches 4471;  Conservative    0;  Mismatches  208;  Indels   43;  Gaps    5;

Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
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Db          1 TTGCCCACTCCCTCTCTGCGCGCTCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGC 60

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
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Db         61 AGACGGCAGAGCTCTGCTCTGCCGGCCCCACCGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120

Qy        121 GCCAACTCCATCACTAGGGGT----------------TCCTGGAGGGGTGGAGTCGTGA 163
              | |||||||||||||||||||                |       |    ||   |||
Db        121 GGCAACTCCATCACTAGGGGTAATCGCGAAGCGCCTCCCACGCTGCCGCGTCAGCGCTGA 180

Qy        164 CGTGAATTACGTCATAGGGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTG-TTTTGC 222
              ||| ||||||||||||||    | | ||||||||||||  ||||||||||||  ||||||
Db        181 CGTAAATTACGTCATAGGG---GAGTGGTCCTGTATTAGCTGTCACGTGAGTGCTTTTGC 237

Qy        223 GACATTTTGCGACACCATGTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGT 282
              |||||||||||||||| |||| ||    |||||| || | ||||||||||  |||| |
Db        238 GACATTTTGCGACACCACGTGGCCATTTAGGGTATATATGGCCGAGTGAGCGAGCAGGAT 297

Qy        283 CTCCATTTTGAAGCGGGAGGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGT 342
              ||||||||||    | |  ||  |          |||||||||| || |||||||| ||
Db        298 CTCCATTTTGACCGCGAAATTTGAACGAGCAGCAGCCATGCCGGGCTTCTACGAGATCGT 357

Qy        343 GATTAAGGTCCCCAGCGACCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAA 402
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Db        358 GATCAAGGTGCCGAGCGACCTGGACGAGCACCTGCCGGGCATTTCTGACTCGTTTGTGAG 417

Qy        403 CTGGGTGGCCGAGAAGGAATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGAT 462
              |||||||||||||||||||||||| |||| || ||||||||||||||||||||||||||
Db        418 CTGGGTGGCCGAGAAGGAATGGGAGCTGCCCCCGGATTCTGACATGGATCTGAATCTGAT 477

Qy        463 TGAGCAGGCACCCCTGACCGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCG 522
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Qy        523 CCGCGTGAGTAAGGCCCCGGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTA 582
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Qy        583 CTTCCACCTCCATATTCTGGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTT 642
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Db        598 CTTCCACCTCCATATTCTGGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTT 657

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Qy        703 GCCCAACTGGTTCGCGGTGACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGT 762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 GCCCAACTGGTTCGCGGTGACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGT 777

Qy        763 GGACGAGTGCTACATCCCCAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGC 822
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Db        778 GGACGAGTGCTACATCCCCAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGC 837

Qy        823 GTGGACTAACATGGAGGAGTATATAAGCGCGTGTTTAAACCTGGCCGAGCGCAAACGGCT 882
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Db        838 GTGGACTAACATGGAGGAGTATATAAGCGCCTGTTTGAACCTGGCCGAGCGCAAACGGCT 897

Qy        883 CGTGGCGCACGACCTGACCCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAA 942
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Db        898 CGTGGCGCAGCACCTGACCCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAA 957

Qy        943 CCCCAATTCTGACGCGCCTGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGT 1002
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Db        958 CCCCAATTCTGACGCGCCTGTCATCCGGTCAAAAACCTCCGCGCGCTACATGGAGCTGGT 1017

Qy       1003 CGGGTGGCTGGTGGACCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGC 1062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1018 CGGGTGGCTGGTGGACCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGC 1077

Qy       1063 CTCGTACATCTCCTTCAACGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGA 1122
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Db       1078 CTCGTACATCTCCTTCAACGCCGCTTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGA 1137

Qy       1123 CAATGCCGGCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGC 1182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 CAATGCCGGCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGC 1197

Qy       1183 TCCGCCCGCCGACATTAAAACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGA 1242
              |||||||| |||||||||||||||||| |||||||||||||||||||||||||||||||||
Db       1198 TCCGCCCGCGGACATTAAAACCAACCGCATCTACCGCATCCTGGAGCTGAACGGCTACGA 1257

Qy       1243 CCCTGCCTACGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAA 1302
              |||||||||||||||||||||||||||||||||||||||||||||||||| || |||||
Db       1258 ACCTGCCTACGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGGAAGCGCAA 1317

Qy       1303 CACCATCTGGCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGC 1362
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1363 CCACGCCGTGCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGA 1422
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
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Qy       1483 GTCCGCCAAGGCCATTCTCGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTC 1542
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Qy       1543 CGCCCAGATCGATCCCACCCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGAT 1602
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Qy       2083 TCGGAAACTCTGTGCCATTCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGC 2142
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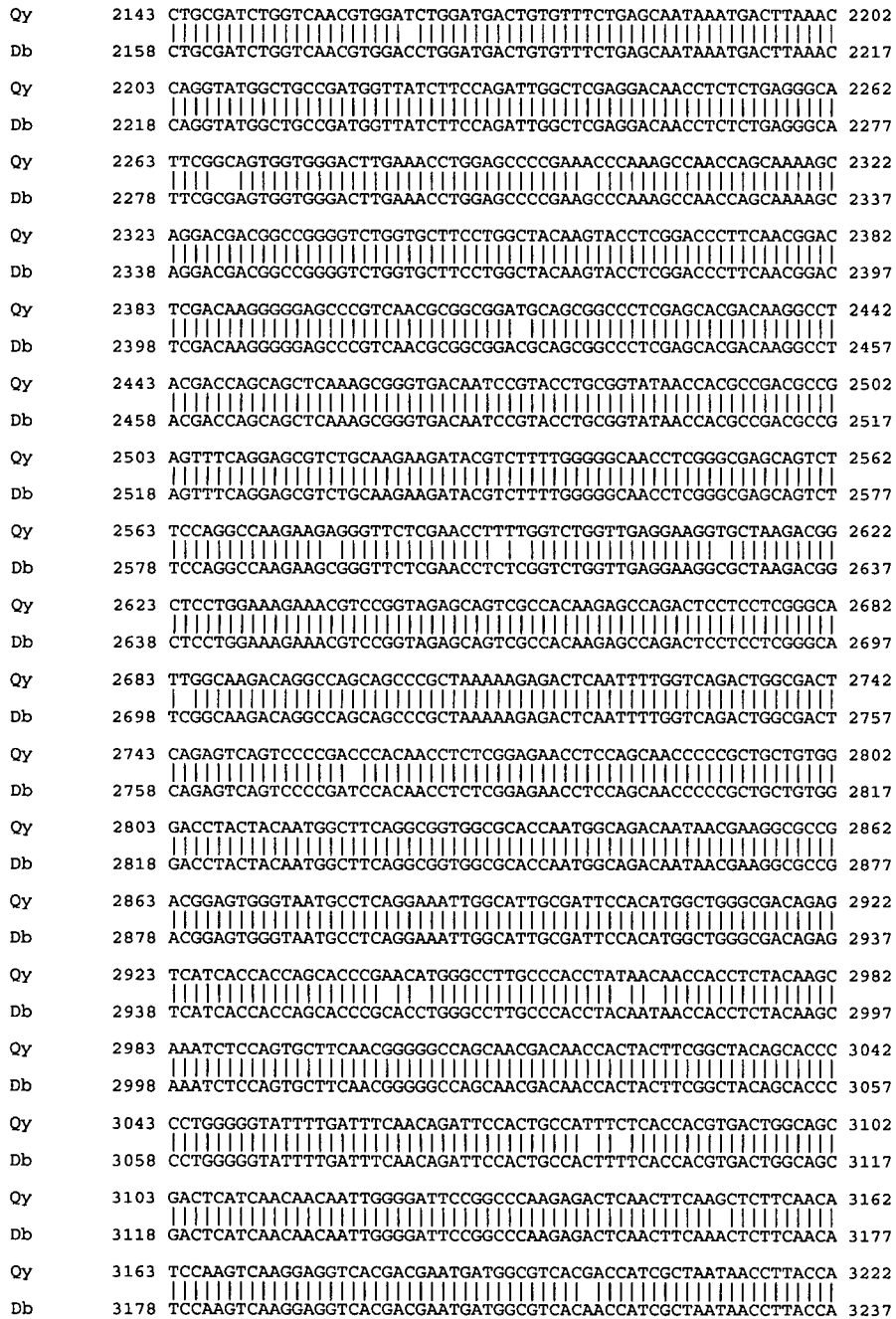
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Db 2518 AGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCT 2577
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; Publication No. US20040057933A1
; GENERAL INFORMATION:
;  APPLICANT: Wilson, James M.
;  APPLICANT:  Xiao, Weidong
;  TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
;  TITLE OF INVENTION:  Vectors and Host Cells Containing Same
;  FILE REFERENCE: GNVPN.031USA
;  CURRENT APPLICATION NUMBER: US/10/696,900
;  CURRENT FILING DATE:  2003-10-30
;  PRIOR APPLICATION NUMBER: US/09/807,802A
;  PRIOR FILING DATE: 2002-02-21
;  PRIOR APPLICATION NUMBER: US 60/107,114
;  PRIOR FILING DATE: 1998-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/25694
;  PRIOR FILING DATE: 1999-11-02
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 4718
;   TYPE: DNA
;   ORGANISM: AAV-1
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (335)..(2206)
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;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2223)..(4430)
;   OTHER INFORMATION:
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Qy       2263 TTCGGCAGTGGTGGGACTTGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGC 2322
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Qy       2323 AGGACGACGGCCGGGGTCTGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGAC 2382
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Qy       2383 TCGACAAGGGGGAGCCCGTCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCT 2442
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Qy       2503 AGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCT 2562
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Db       2518 AGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCT 2577

Qy       2563 TCCAGGCCAAGAAGAGGGTTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGG 2622
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Qy       2623 CTCCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCA 2682
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Qy       2683 TTGGCAAGACAGGCCAGCAGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACT 2742
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Qy       2743 CAGAGTCAGTCCCCGACCCACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGG 2802
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Qy       2803 GACCTACTACAATGGCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCG 2862
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Db       2818 GACCTACTACAATGGCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCG 2877

Qy       2863 ACGGAGTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAG 2922
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Db       2998 AAATCTCCAGTGCTTCAACGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCC 3057

Qy       3043 CCTGGGGGTATTTTGATTTCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGC 3102
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Qy       3283 ACCAGGGCTGCCTCCCTCCGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACC 3342
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Qy       3943 CTGTGGCAGTCAATCTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTA 4002

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Qy       4003 TGGGAGCCTTACCTGGAATGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTT 4062

Db       4018 TGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTT 4077

Qy       4063 GGGCCAAAATTCCTCACACGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTG 4122

Db       4078 GGGCCAAAATTCCTCACACAGATGGACACTTTCACCCGTCTCCTCTTATGGGCGGCTTTG 4137

Qy       4123 GACTTAAGCACCCGCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTC 4182

Db       4138 GACTCAAGAACCCGCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTC 4197

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RESULT 11
US-10-427-129-1
; Sequence 1, Application US/10427129
; Publication No. US20040101514A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Yuhong
;  APPLICANT:  Luo, Jia
;  APPLICANT:  During, Matthew
;  TITLE OF INVENTION: High Transgene Expression of A Pseudotyped Adeno-Associated Virus
;  FILE REFERENCE: 102182-24
;  CURRENT APPLICATION NUMBER: US/10/427,129
;  CURRENT FILING DATE:  2003-05-01
;  PRIOR APPLICATION NUMBER: 09/804,898
;  PRIOR FILING DATE: 2001-03-13
;  PRIOR APPLICATION NUMBER: 60/189,110
;  PRIOR FILING DATE: 2000-03-14
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 4718
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US-10-427-129-1

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  Matches 4471;  Conservative    0;  Mismatches  208;  Indels   43;  Gaps    5;

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Qy        121 GCCAACTCCATCACTAGGGGT----------------TCCTGGAGGGGTGGAGTCGTGA 163

Db        121 GGCAACTCCATCACTAGGGGTAATCGCGAAGCGCCTCCCACGCTGCCGCGTCAGCGCTGA 180

Qy        164 CGTGAATTACGTCATAGGGGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTG-TTTTGC 222

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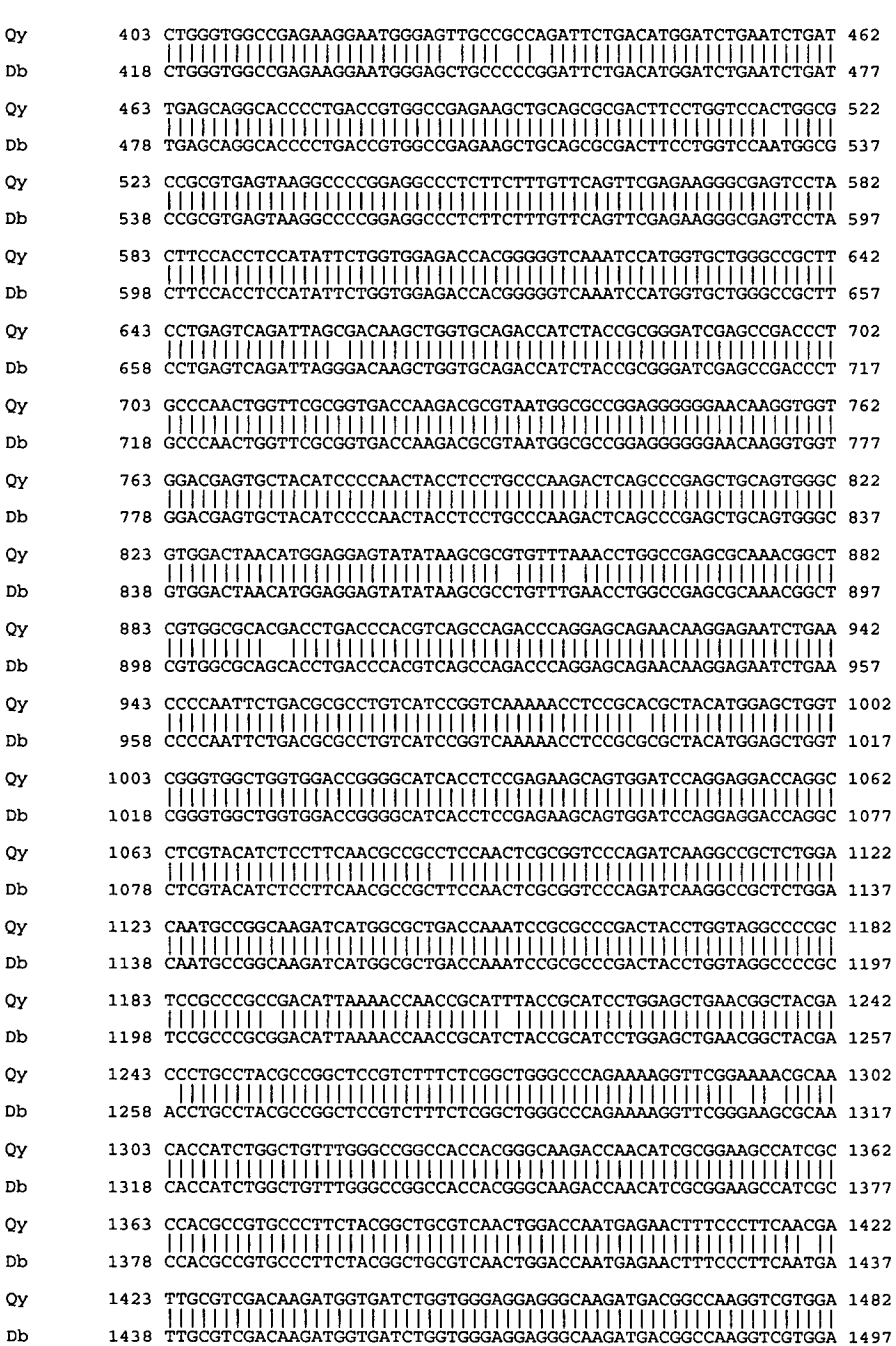
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Qy 763 GGACGAGTGCTACATCCCCAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGC 822
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Qy 1603 TGACGGGAACAGCACCACCTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATT 1662
Db 1618 TGACGGGAACAGCACCACCTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATT 1677
Qy 1663 TGAACTCACCCGCCGTCTGGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGA 1722
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Db 1858 CTGCCCCTCAGTCGCGGATCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGC 1917
Qy 1903 CGACAGGTACCAAAACAAATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTG 1962
Db 1918 CGACAGGTACCAAAACAAATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTG 1977
Qy 1963 CAAAACATGCGAGAGAATGAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGA 2022
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Qy 2203 CAGGTATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCA 2262
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Qy 2323 AGGACGACGGCCGGGGTCTGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGAC 2382
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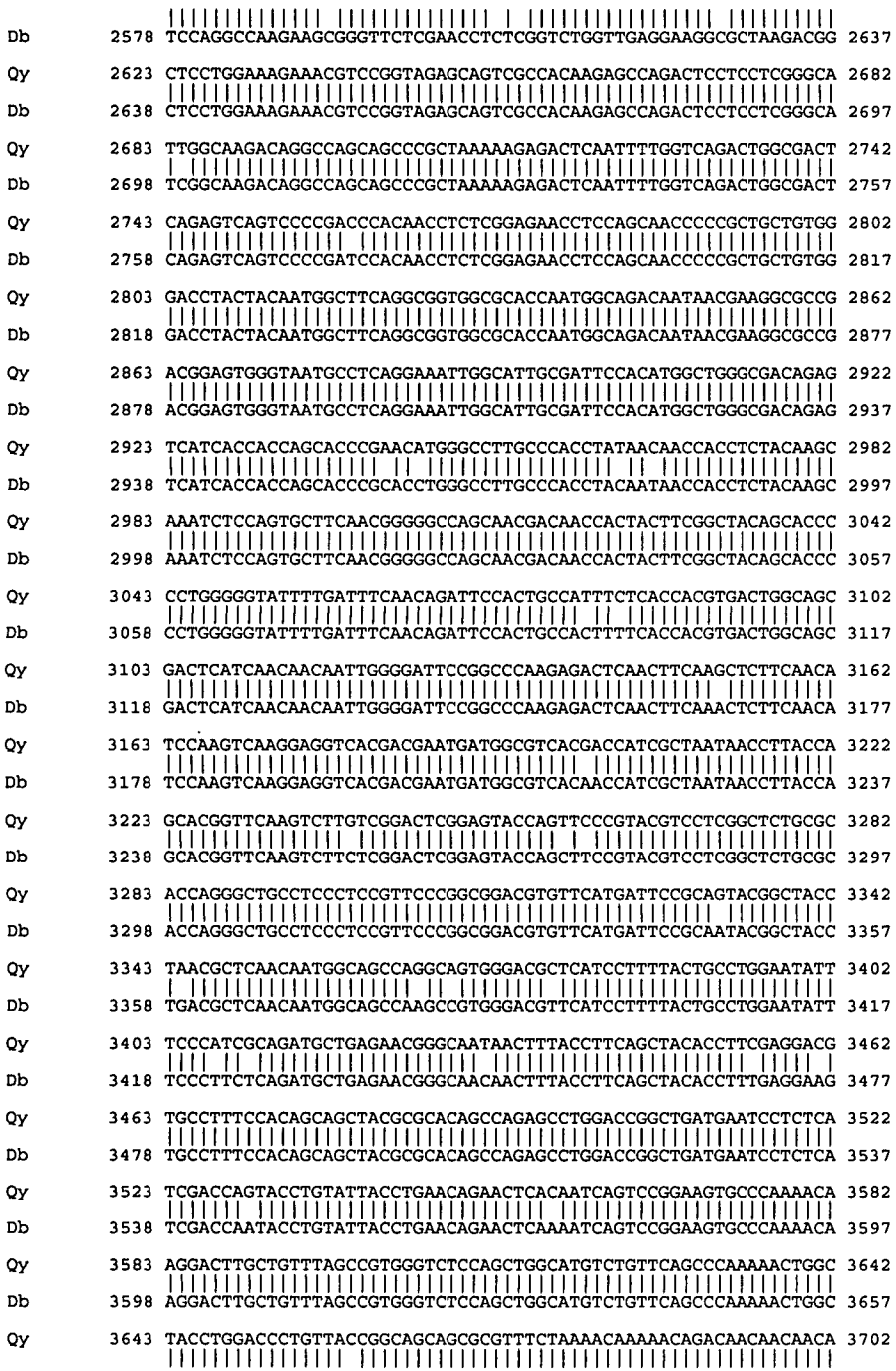

RESULT 12
US-10-959-017-3

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; Sequence 3, Application US/10959017
; Publication No. US20050106125A1
; GENERAL INFORMATION:
;  APPLICANT: FALCK-PEDERSEN, ERIK S
;  APPLICANT:  PHILPOTT, NICOLA
;  TITLE OF INVENTION: USE OF AAV INTEGRATION EFFICIENCY ELEMENT FOR MEDIATING
;  TITLE OF INVENTION:  SITE-SPECIFIC INTEGRATION OF A TRANSCRIPTION UNIT
;  FILE REFERENCE: 230526
;  CURRENT APPLICATION NUMBER: US/10/959,017
;  CURRENT FILING DATE:  2004-10-05
;  PRIOR APPLICATION NUMBER: PCT/US03/11191
;  PRIOR FILING DATE: 2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/371,044
;  PRIOR FILING DATE: 2002-04-09
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 4718
;   TYPE: DNA
;   ORGANISM: adeno-associated virus serotype 1
US-10-959-017-3

  Query Match             90.8%;  Score 4253.2;  DB 10;  Length 4718;
  Best Local Similarity   94.7%;  Pred. No. 0;
  Matches 4471;  Conservative    0;  Mismatches  208;  Indels   43;  Gaps    5;

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              | |||||||||||||||||                |       |    ||   |||
Db        121 GGCAACTCCATCACTAGGGGTAATCGCGAAGCGCCTCCCACGCTGCCGCGTCAGCGCTGA 180

Qy        164 CGTGAATTACGTCATAGGGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTG-TTTTGC 222
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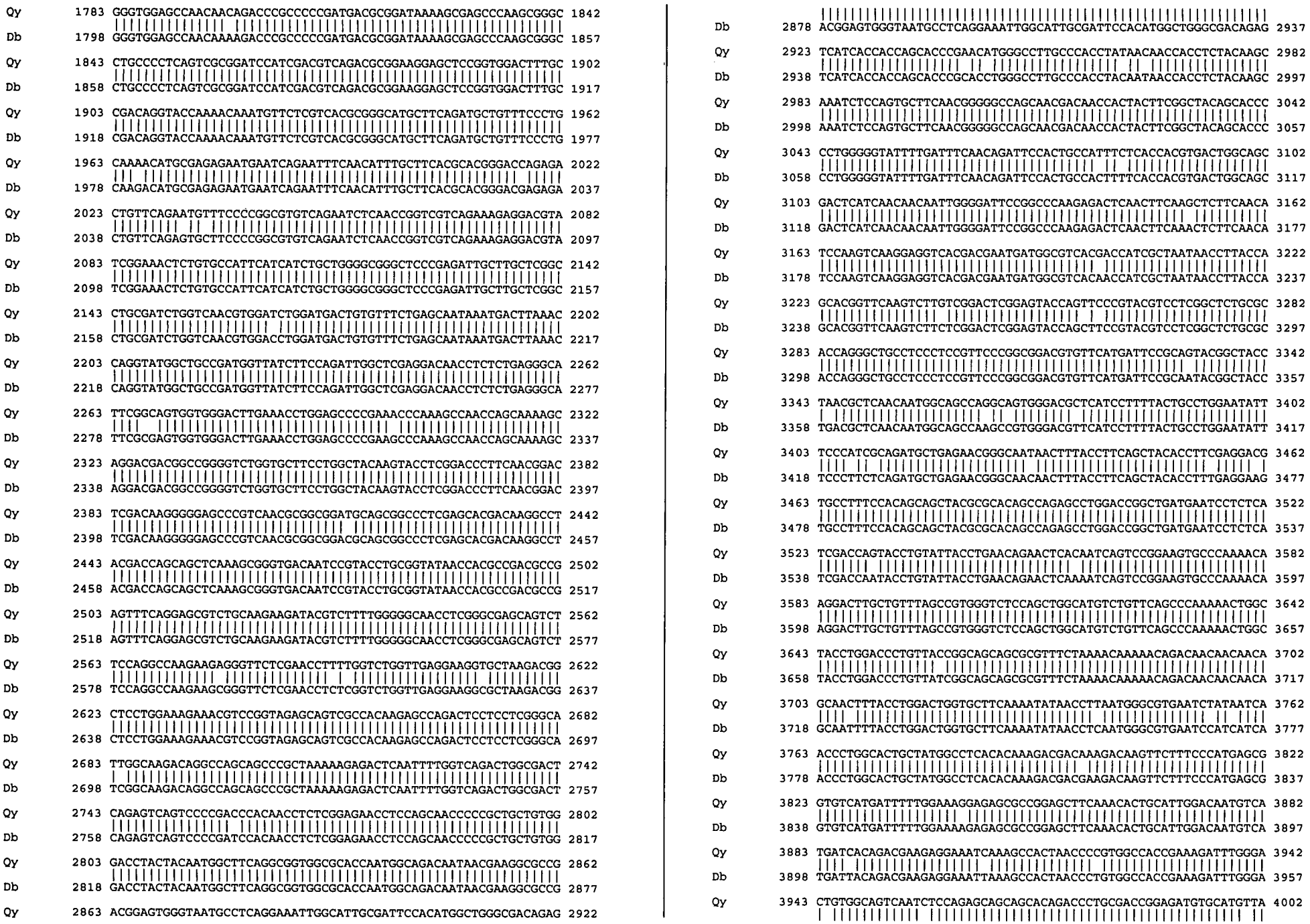
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;  TITLE OF INVENTION: AAV VECTORS AND METHODS
;  FILE REFERENCE: 28335/41335
;  CURRENT APPLICATION NUMBER: US/11/145,035
;  CURRENT FILING DATE:  2005-06-03
;  PRIOR APPLICATION NUMBER: US 10/038,972
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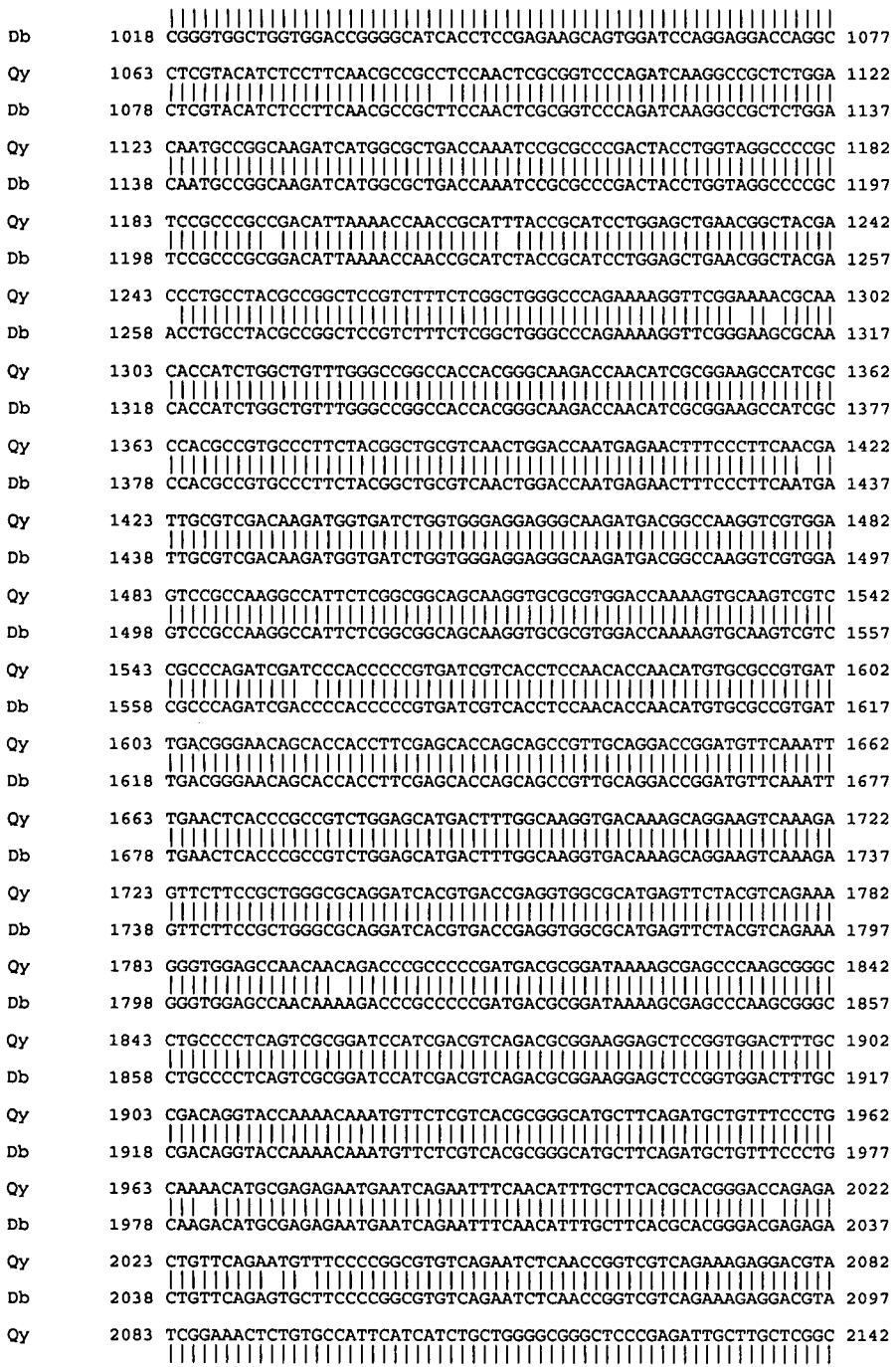
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RESULT 14
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; Sequence 1, Application US/10291583
; Publication No. US20030138772A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Guangping
; APPLICANT: Wilson, James M.
; APPLICANT: Alvira, Mauricio
; TITLE OF INVENTION: A Method of Detecting and/or Identifying Adeno-Associated Virus (A
; TITLE OF INVENTION: Sequences and Isolating No. US20030138772A1el Sequences Identifie
; FILE REFERENCE: UPN-02735USA
; CURRENT APPLICATION NUMBER: US/10/291,583
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/350,607
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/341,117
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/377,066
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 60/386,675
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4721
; TYPE: DNA
; ORGANISM: adeno-associated virus serotype 7
US-10-291-583-1

Query Match 78.5%; Score 3678.4; DB 7; Length 4721;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 4135; Conservative 0; Mismatches 541; Indels 52; Gaps 8;

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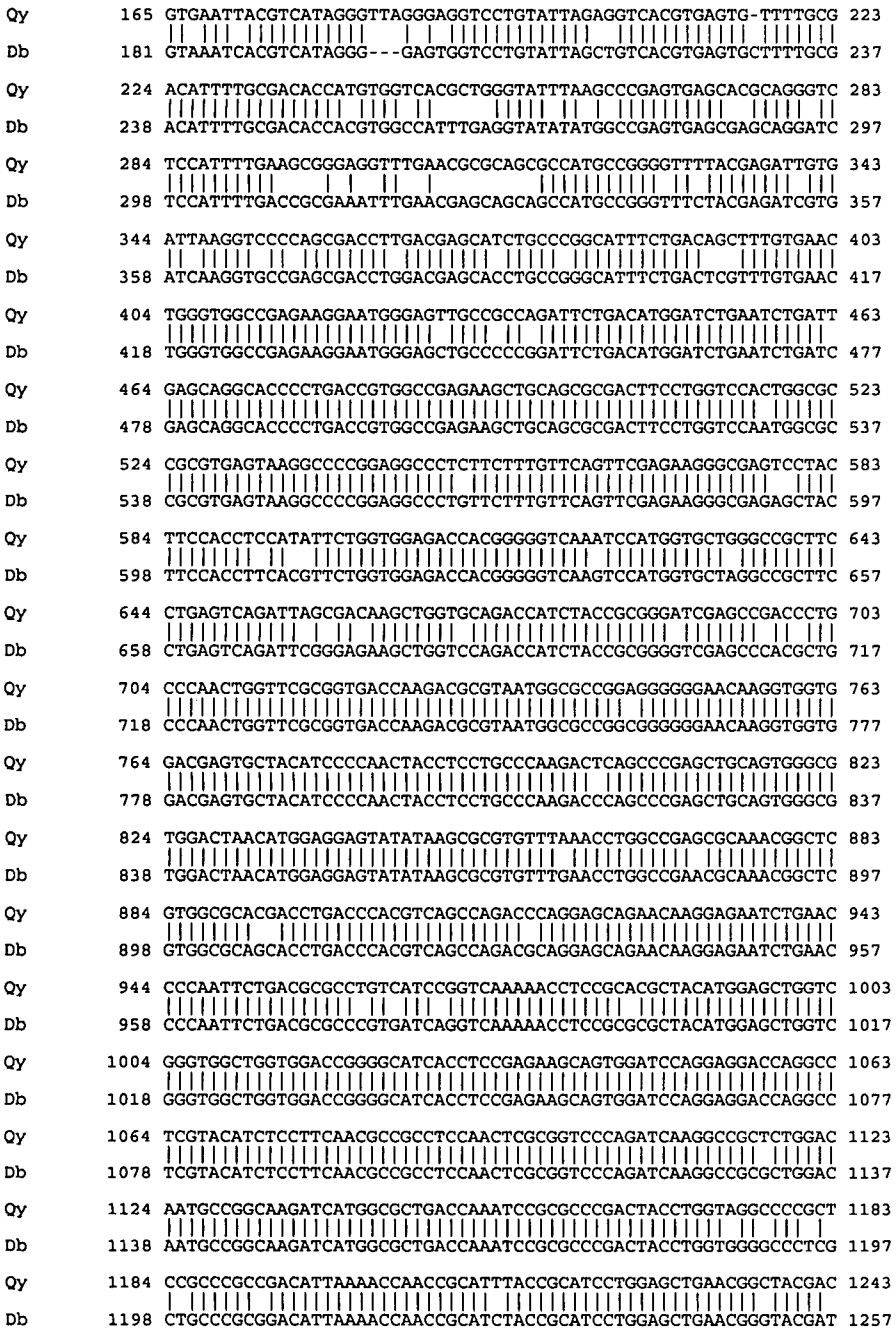
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RESULT 15
US-11-145-035-37
; Sequence 37, Application US/11145035
; Publication No. US20050287122A1
; GENERAL INFORMATION:
;  APPLICANT: Bartlett et al.
;  TITLE OF INVENTION: AAV VECTORS AND METHODS
;  FILE REFERENCE: 28335/41335
;  CURRENT APPLICATION NUMBER: US/11/145,035
;  CURRENT FILING DATE:  2005-06-03
;  PRIOR APPLICATION NUMBER: US 10/038,972
;  PRIOR FILING DATE: 2002-01-04
;  PRIOR APPLICATION NUMBER: US 60/260,124
;  PRIOR FILING DATE: 2001-01-05
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
;   LENGTH: 4721
;   TYPE: DNA
;   ORGANISM: Adeno-associated virus 7
US-11-145-035-37

  Query Match             78.5%;  Score 3678.4;  DB 15;  Length 4721;
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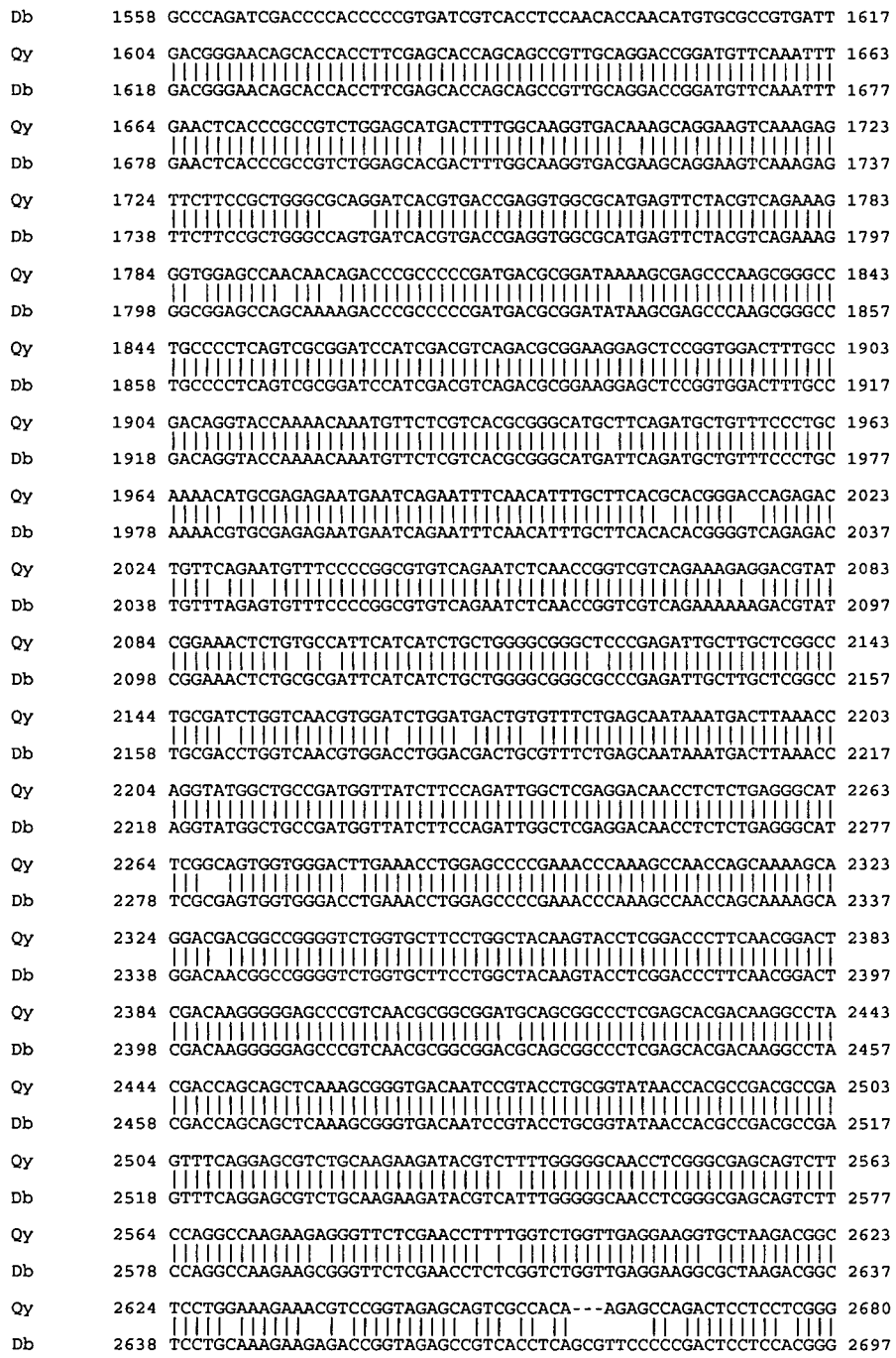
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	3296.2	70.4	4679	3	US-10-038-972A-12	Sequence 12, Appl
	4	3296.2	70.4	8698	3	US-09-770-315-2	Sequence 2, Appli
	5	3293	70.3	4679	4	US-09-717-789C-25	Sequence 25, Appl
	6	3270.8	69.8	4680	2	US-08-254-358-1	Sequence 1, Appli
	7	3270.8	69.8	4680	2	US-08-475-391-1	Sequence 1, Appli
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	14	3114.4	66.5	7557	3	US-09-770-315-3	Sequence 3, Appli
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ALIGNMENTS

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; Sequence 19, Application US/09807802A
; Patent No. 6759237
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; APPLICANT: Xiao, Weidong
; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
; TITLE OF INVENTION: Vectors and Host Cells Containing Same
; FILE REFERENCE: GNVPN.031USA
; CURRENT APPLICATION NUMBER: US/09/807,802A
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/107,114
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/25694
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 4683
; TYPE: DNA
; ORGANISM: AAV-6
US-09-807-802A-19

Query Match 100.0%; Score 4683; DB 3; Length 4683;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       3121 GGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCA 3180

Qy       3181 CGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTGT 3240
Db       3181 CGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTGT 3240

Qy       3241 CGGACTCGGAGTACCAGTTCCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTC 3300
Db       3241 CGGACTCGGAGTACCAGTTCCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTC 3300

Qy       3301 CGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCA 3360
Db       3301 CGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCA 3360

Qy       3361 GCCAGGCAGTGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGA 3420
Db       3361 GCCAGGCAGTGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGA 3420

Qy       3421 GAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCT 3480
Db       3421 GAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCT 3480

Qy       3481 ACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATT 3540
Db       3481 ACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATT 3540

Qy       3541 ACCTGAACAGAACTCACAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCC 3600
Db       3541 ACCTGAACAGAACTCACAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCC 3600

Qy       3601 GTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACC 3660
Db       3601 GTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACC 3660

Qy       3661 GGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTG 3720
Db       3661 GGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTG 3720

Qy       3721 GTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGG 3780
Db       3721 GTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGG 3780

Qy       3781 CCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAA 3840
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Db       3841 AGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGG 3900

Qy       3901 AAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCC 3960
Db       3901 AAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCC 3960

Qy       3961 AGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAA 4020
Db       3961 AGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAA 4020

Qy       4021 TGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACA 4080
Db       4021 TGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACA 4080

Qy       4081 CGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTC 4140
Db       4081 CGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTC 4140

Qy       4141 CTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTA 4200
Db       4141 CTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTA 4200

Qy       4201 CAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAAT 4260
Db       4201 CAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAAT 4260

Qy       4261 GGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACT 4320
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Qy       4321 ATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTC 4380
Db       4321 ATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTC 4380

Qy       4381 GCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCG 4440
Db       4381 GCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCG 4440

Qy       4441 GTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCACCATA 4500
Db       4441 GTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCACCATA 4500

Qy       4501 GCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGAATACCCCTAGTGATGGAGTT 4560
Db       4501 GCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGAATACCCCTAGTGATGGAGTT 4560

Qy       4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCG 4620
Db       4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCG 4620

Qy       4621 TCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGC 4680
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Db       4621 TCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGC 4680

Qy       4681 CAA 4683
              |||
Db       4681 CAA 4683


RESULT 2
US-09-807-802A-1
; Sequence 1, Application US/09807802A
; Patent No. 6759237
; GENERAL INFORMATION:
;  APPLICANT: Wilson, James M.
;  APPLICANT:  Xiao, Weidong
;  TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
;  TITLE OF INVENTION:  Vectors and Host Cells Containing Same
;  FILE REFERENCE: GNVPN.031USA
;  CURRENT APPLICATION NUMBER: US/09/807,802A
;  CURRENT FILING DATE:  2002-02-21
;  PRIOR APPLICATION NUMBER: US 60/107,114
;  PRIOR FILING DATE: 1998-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/25694
;  PRIOR FILING DATE: 1999-11-02
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 4718
;   TYPE: DNA
;   ORGANISM: AAV-1
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (335)..(2206)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2223)..(4430)
;   OTHER INFORMATION:
US-09-807-802A-1

  Query Match             90.8%;  Score 4253.2;  DB 3;  Length 4718;
  Best Local Similarity   94.7%;  Pred. No. 0;
  Matches 4471;  Conservative    0;  Mismatches  208;  Indels   43;  Gaps    5;

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              ||| |||||||||||||||||||||||||||||||  || |||| |  ||||||||||| |
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Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
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              | |||||||||||||||||||                |       |    ||   |||
Db        121 GGCAACTCCATCACTAGGGGTAATCGCGAAGCGCCTCCCACGCTGCCGCGTCAGCGCTGA 180

Qy        164 CGTGAATTACGTCATAGGGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTG-TTTTGC 222
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Db        181 CGTAAATTACGTCATAGGG---GAGTGGTCCTGTATTAGCTGTCACGTGAGTGCTTTTGC 237

Qy        223 GACATTTTGCGACACCATGTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGT 282
              |||||||||||||||| |||| ||    |||||| || | ||||||||||  ||||| |
Db        238 GACATTTTGCGACACCACGTGGCCATTTAGGGTATATATGGCCGAGTGAGCGAGCAGGAT 297

Qy        283 CTCCATTTTGAAGCGGGAGGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGT 342
              ||||||||||    | |  ||  |          |||||||||| || ||||||| ||
Db        298 CTCCATTTTGACCGCGAAATTTGAACGAGCAGCAGCCATGCCGGGCTTCTACGAGATCGT 357

Qy        343 GATTAAGGTCCCCAGCGACCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAA 402
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Db        358 GATCAAGGTGCCGAGCGACCTGGACGAGCACCTGCCGGGCATTTCTGACTCGTTTGTGAG 417

Qy        403 CTGGGTGGCCGAGAAGGAATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGAT 462
              |||||||||||||||||||||||| |||| || ||||||||||||||||||||||||||

Db        418 CTGGGTGGCCGAGAAGGAATGGGAGCTGCCCCCGGATTCTGACATGGATCTGAATCTGAT 477

Qy        463 TGAGCAGGCACCCCTGACCGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCG 522
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        478 TGAGCAGGCACCCCTGACCGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCAATGGCG 537

Qy        523 CCGCGTGAGTAAGGCCCCGGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTA 582
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Db        538 CCGCGTGAGTAAGGCCCCGGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTA 597

Qy        583 CTTCCACCTCCATATTCTGGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTT 642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 CTTCCACCTCCATATTCTGGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTT 657

Qy        643 CCTGAGTCAGATTAGCGACAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCT 702
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        658 CCTGAGTCAGATTAGGGACAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCT 717

Qy        703 GCCCAACTGGTTCGCGGTGACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGT 762
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Db        718 GCCCAACTGGTTCGCGGTGACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGT 777

Qy        763 GGACGAGTGCTACATCCCCAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGC 822
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Db        838 GTGGACTAACATGGAGGAGTATATAAGCGCCTGTTTGAACCTGGCCGAGCGCAAACGGCT 897

Qy        883 CGTGGCGCACGACCTGACCCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAA 942
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 CGTGGCGCAGCACCTGACCCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAA 957

Qy        943 CCCCAATTCTGACGCGCCTGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGT 1002
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        958 CCCCAATTCTGACGCGCCTGTCATCCGGTCAAAAACCTCCGCGCGCTACATGGAGCTGGT 1017

Qy       1003 CGGGTGGCTGGTGGACCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGC 1062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 CGGGTGGCTGGTGGACCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGC 1077

Qy       1063 CTCGTACATCTCCTTCAACGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGA 1122
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Db       1078 CTCGTACATCTCCTTCAACGCCGCTTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGA 1137

Qy       1123 CAATGCCGGCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGC 1182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 CAATGCCGGCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGC 1197

Qy       1183 TCCGCCCGCCGACATTAAAACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGA 1242
              ||||||||| |||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1198 TCCGCCCGCGGACATTAAAACCAACCGCATCTACCGCATCCTGGAGCTGAACGGCTACGA 1257

Qy       1243 CCCTGCCTACGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAA 1302
              |||||||||||||||||||||||||||||||||||||||||||||||||||| || |||||
Db       1258 ACCTGCCTACGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGGAAGCGCAA 1317

Qy       1303 CACCATCTGGCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGC 1362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1318 CACCATCTGGCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGC 1377

Qy       1363 CCACGCCGTGCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGA 1422
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1378 CCACGCCGTGCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAATGA 1437

Qy       1423 TTGCGTCGACAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGA 1482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1438 TTGCGTCGACAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGA 1497

Qy       1483 GTCCGCCAAGGCCATTCTCGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTC 1542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1498 GTCCGCCAAGGCCATTCTCGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTC 1557
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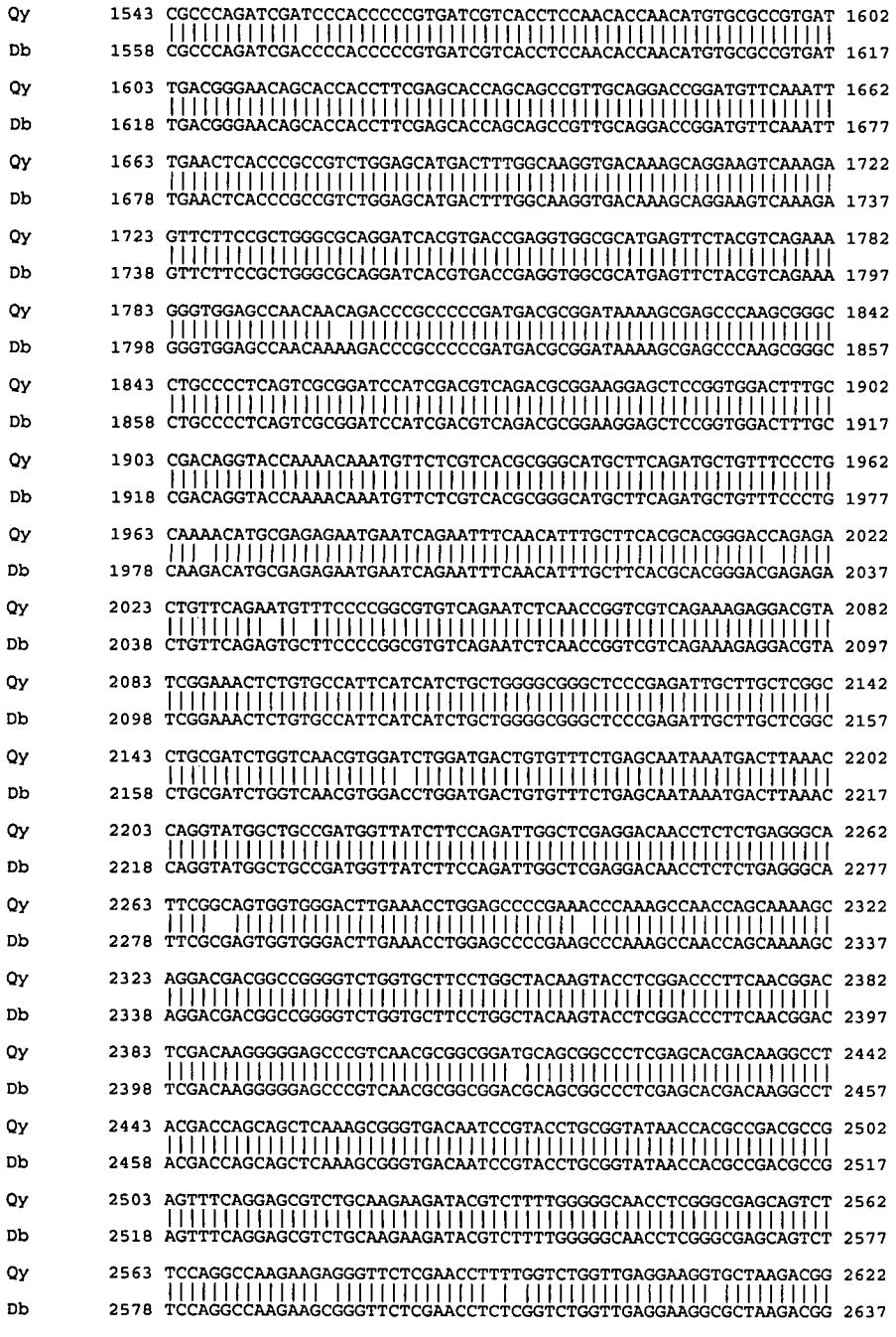
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Db 1558 CGCCCAGATCGACCCCACCCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGAT 1617
Qy 1603 TGACGGGAACAGCACCACCTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATT 1662
Db 1618 TGACGGGAACAGCACCACCTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATT 1677
Qy 1663 TGAACTCACCCGCCGTCTGGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGA 1722
Db 1678 TGAACTCACCCGCCGTCTGGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGA 1737
Qy 1723 GTTCTTCCGCTGGGCGCAGGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAA 1782
Db 1738 GTTCTTCCGCTGGGCGCAGGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAA 1797
Qy 1783 GGGTGGAGCCAACAACAGACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGC 1842
Db 1798 GGGTGGAGCCAACAAAAGACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGC 1857
Qy 1843 CTGCCCCTCAGTCGCGGATCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGC 1902
Db 1858 CTGCCCCTCAGTCGCGGATCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGC 1917
Qy 1903 CGACAGGTACCAAAACAAATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTG 1962
Db 1918 CGACAGGTACCAAAACAAATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTG 1977
Qy 1963 CAAAACATGCGAGAGAATGAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGA 2022
Db 1978 CAAGACATGCGAGAGAATGAATCAGAATTTCAACATTTGCTTCACGCACGGGACGAGAGA 2037
Qy 2023 CTGTTCAGAATGTTTCCCCGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTA 2082
Db 2038 CTGTTCAGAGTGCTTCCCCGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTA 2097
Qy 2083 TCGGAAACTCTGTGCCATTCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGC 2142
Db 2098 TCGGAAACTCTGTGCCATTCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGC 2157
Qy 2143 CTGCGATCTGGTCAACGTGGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAAC 2202
Db 2158 CTGCGATCTGGTCAACGTGGACCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAAC 2217
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Db 2218 CAGGTATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCA 2277
Qy 2263 TTCGGCAGTGGTGGGACTTGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGC 2322
Db 2278 TTCGCGAGTGGTGGGACTTGAAACCTGGAGCCCCGAAGCCCAAAGCCAACCAGCAAAAGC 2337
Qy 2323 AGGACGACGGCCGGGGTCTGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGAC 2382
Db 2338 AGGACGACGGCCGGGGTCTGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGAC 2397
Qy 2383 TCGACAAGGGGGAGCCCGTCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCT 2442
Db 2398 TCGACAAGGGGGAGCCCGTCAACGCGGCGGACGCAGCGGCCCTCGAGCACGACAAGGCCT 2457
Qy 2443 ACGACCAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCG 2502
Db 2458 ACGACCAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCG 2517
Qy 2503 AGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCT 2562
Db 2518 AGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCT 2577
Qy 2563 TCCAGGCCAAGAAGAGGGTTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGG 2622
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Qy 2623 CTCCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCA 2682
Db 2638 CTCCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCA 2697
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Db 2818 GACCTACTACAATGGCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCG 2877
Qy 2863 ACGGAGTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAG 2922
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Qy 2983 AAATCTCCAGTGCTTCAACGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCC 3042
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Qy 3163 TCCAAGTCAAGGAGGTCACGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCA 3222
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Db       3718 GCAATTTTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGGCGTGAATCCATCATCA 3777

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Qy       4423 GTGTTAATCAATAAACCGGTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTA 4482

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RESULT 3
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; Sequence 12, Application US/10038972A
; Patent No. 6962815
; GENERAL INFORMATION:
;  APPLICANT: J. Bartlett
;  TITLE OF INVENTION: AAV VECTORS AND METHODS
;  FILE REFERENCE: 28335/36996US
;  CURRENT APPLICATION NUMBER: US/10/038,972A
;  CURRENT FILING DATE:  2002-01-04
;  PRIOR APPLICATION NUMBER: US 60/260,124
;  PRIOR FILING DATE: 2001-01-05
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 4679
;   TYPE: DNA
;   ORGANISM: adeno-associated virus 2
US-10-038-972A-12

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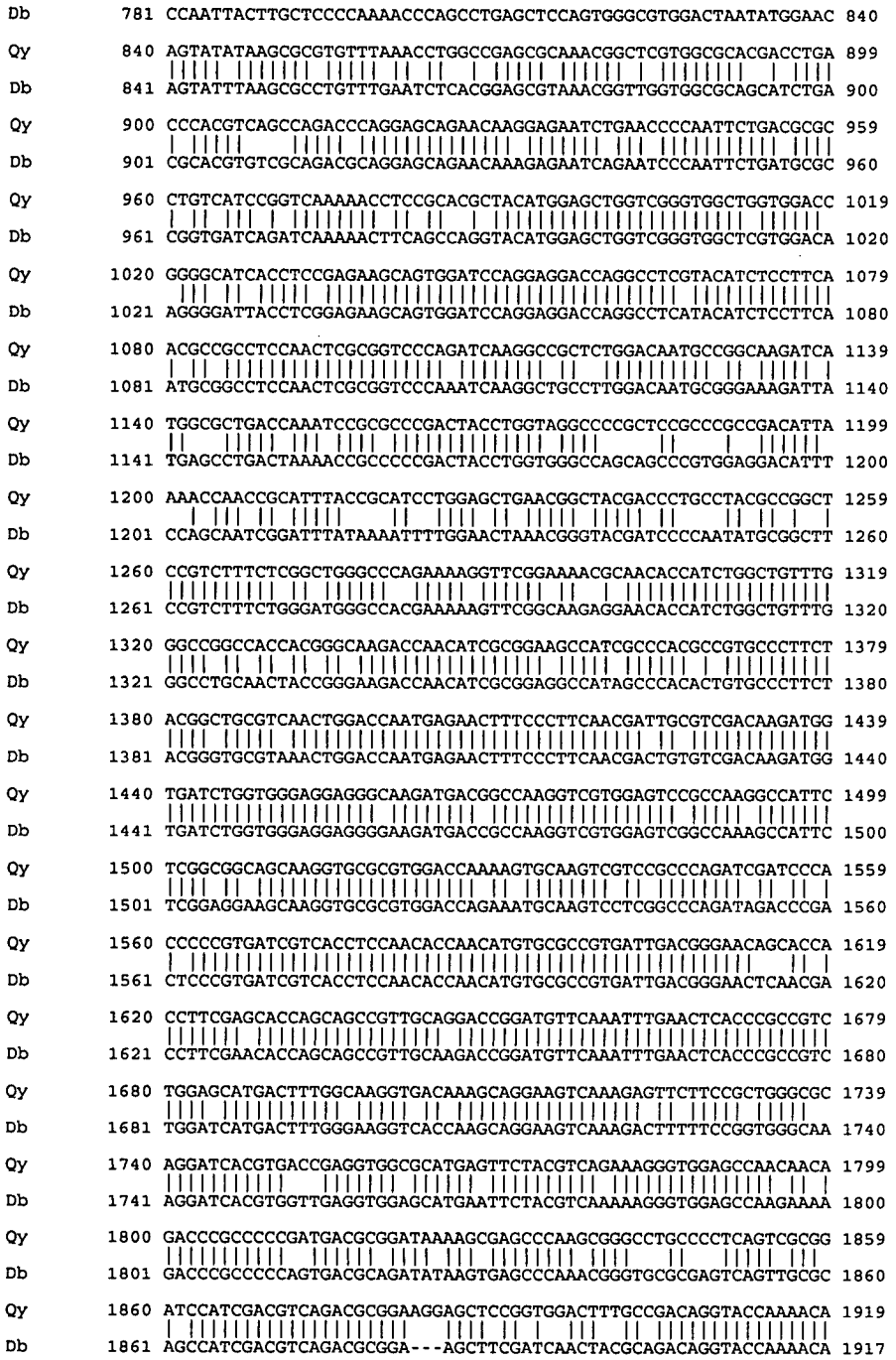
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Db 2212 GATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATAAGACAGTGGTGG 2271
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RESULT 4
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; Sequence 2, Application US/09770315
; Patent No. 6429001
; GENERAL INFORMATION:
; APPLICANT: Chiron Corporation
; TITLE OF INVENTION: Recombinant AAV Packaging Systems
; FILE REFERENCE: 20263-501
; CURRENT APPLICATION NUMBER: US/09/770,315
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,536
; PRIOR FILING DATE: 2000-01-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 8698
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: recombinant DNA
US-09-770-315-2

Query Match 70.4%; Score 3296.2; DB 3; Length 8698;
Best Local Similarity 82.5%; Pred. No. 0;
Matches 3868; Conservative 0; Mismatches 803; Indels 20; Gaps 7;

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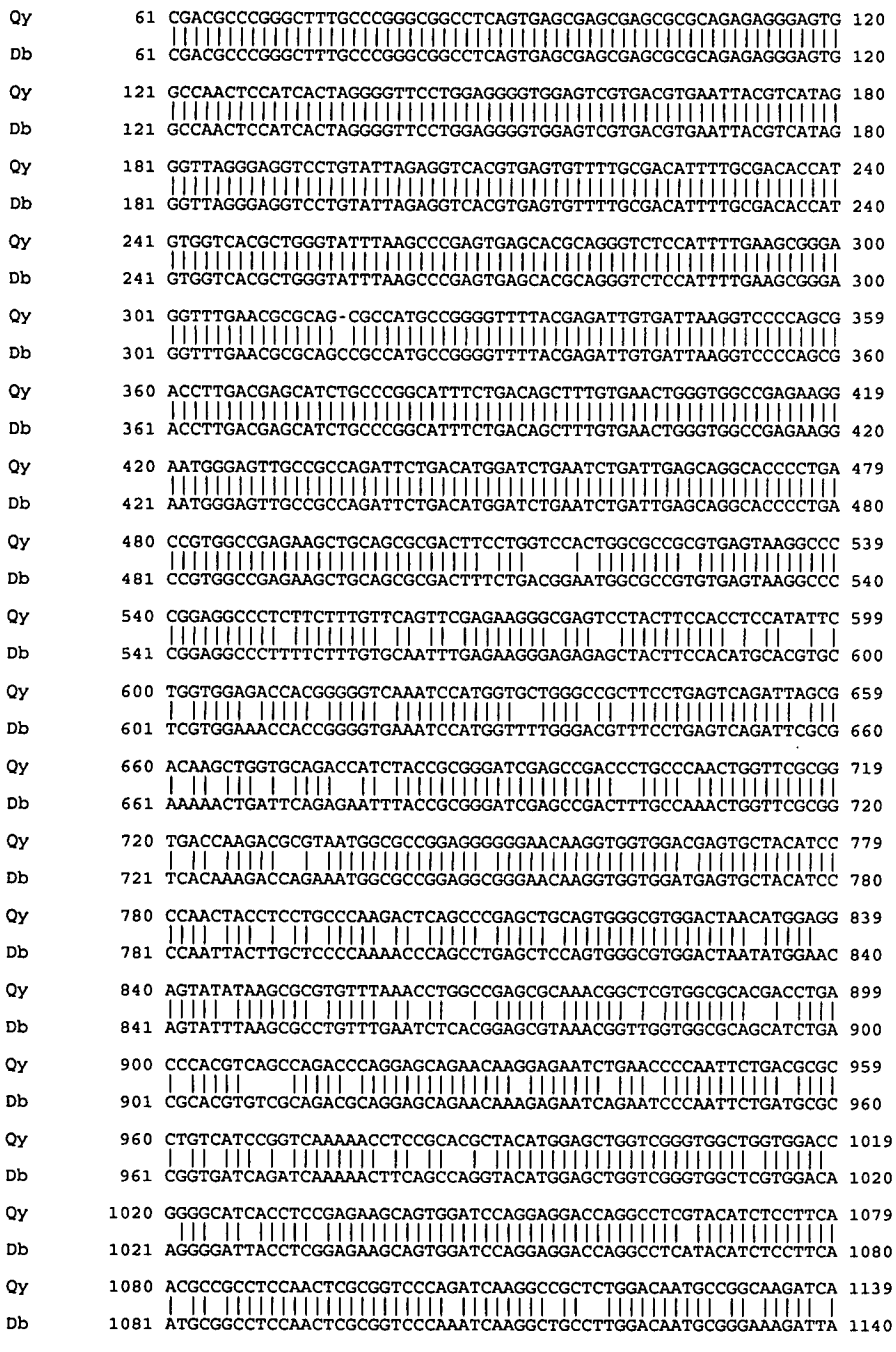

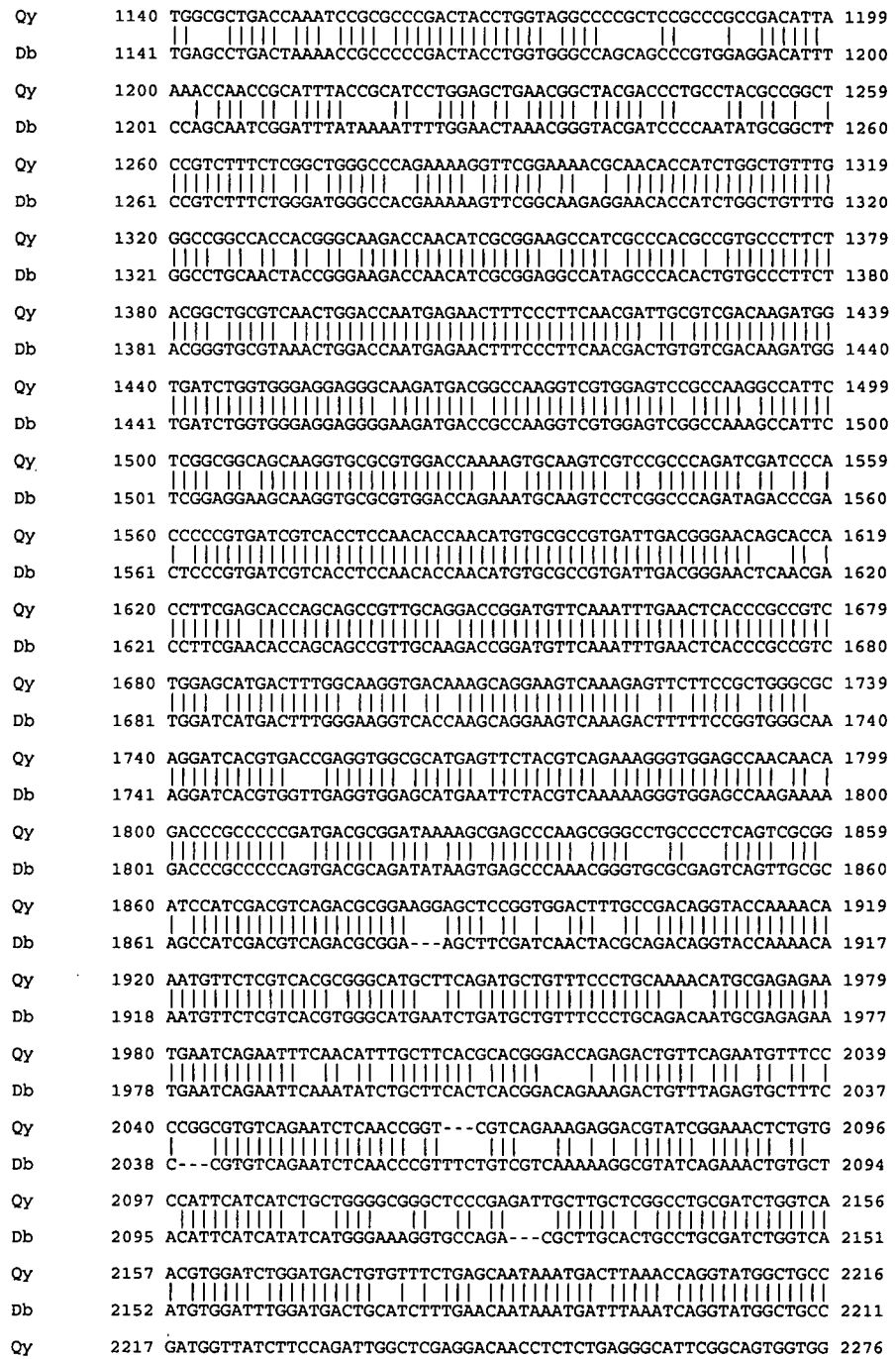

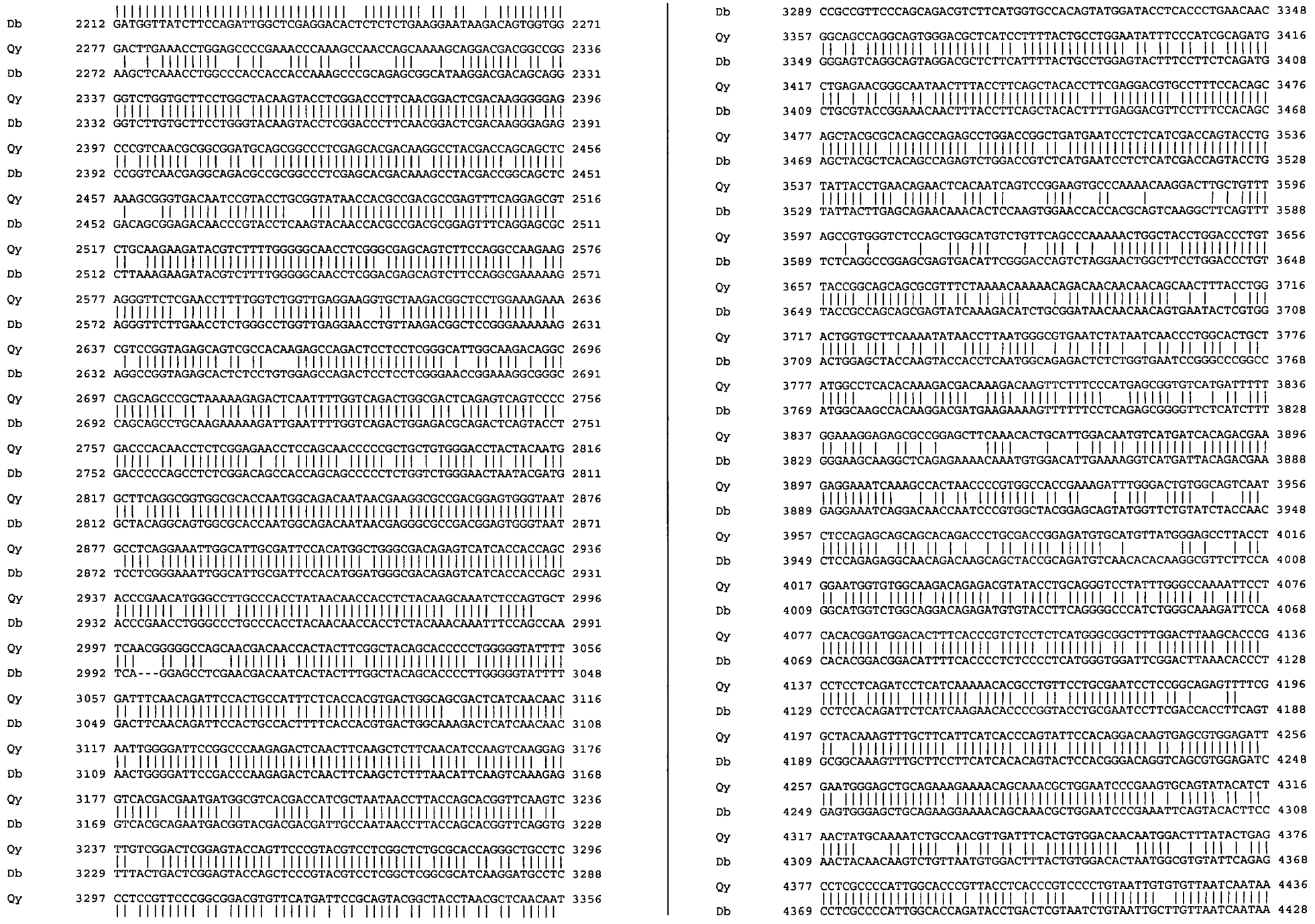

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Db       4429 ACCGTTTAATTCGTTTCAGTTGAACTTTGGTCTCTGCGTATTTCTTTCTTATCTAGTTTC 4488

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Db       4549 ATGGAGTTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAG 4608

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Db       4609 GTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAG 4668

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RESULT 5
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; Sequence 25, Application US/09717789C
; Patent No. 6984517
; GENERAL INFORMATION:
;  APPLICANT: Chiorini, John
;  APPLICANT:  Kotin, Robert M.
;  APPLICANT:  Safer, Brian
;  TITLE OF INVENTION: AAV5 VECTOR AND USES THEREOF
;  FILE REFERENCE: 14014.0323U3
;  CURRENT APPLICATION NUMBER: US/09/717,789C
;  CURRENT FILING DATE:  2000-11-21
;  PRIOR APPLICATION NUMBER: PCT/US99/11958
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/087,029
;  PRIOR FILING DATE: 1998-05-28
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 4679
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
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;   OTHER INFORMATION: Description of Artificial Sequence; No. 6984517e =
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US-09-717-789C-25

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              |||| || || || || |||||||||||||||| ||||| |||||| | ||||||||||
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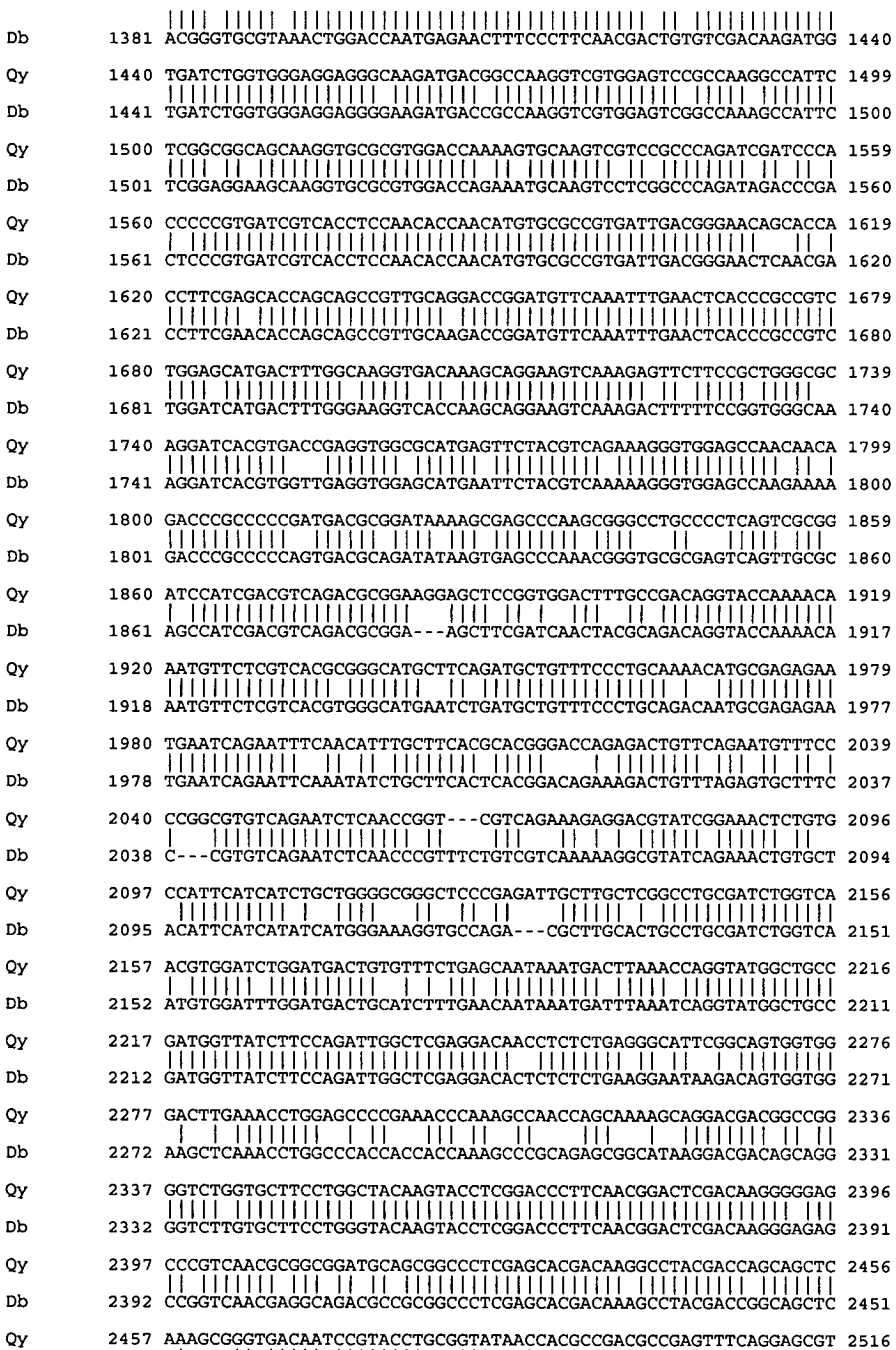
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; Patent No. 5658785
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;    APPLICANT:  Johnson, Philip R.
;    TITLE OF INVENTION:  Adeno-Associated Virus Materials and
;    TITLE OF INVENTION:  Methods
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 S. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/254,358
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5658785and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31975
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  1:
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US-08-254-358-1

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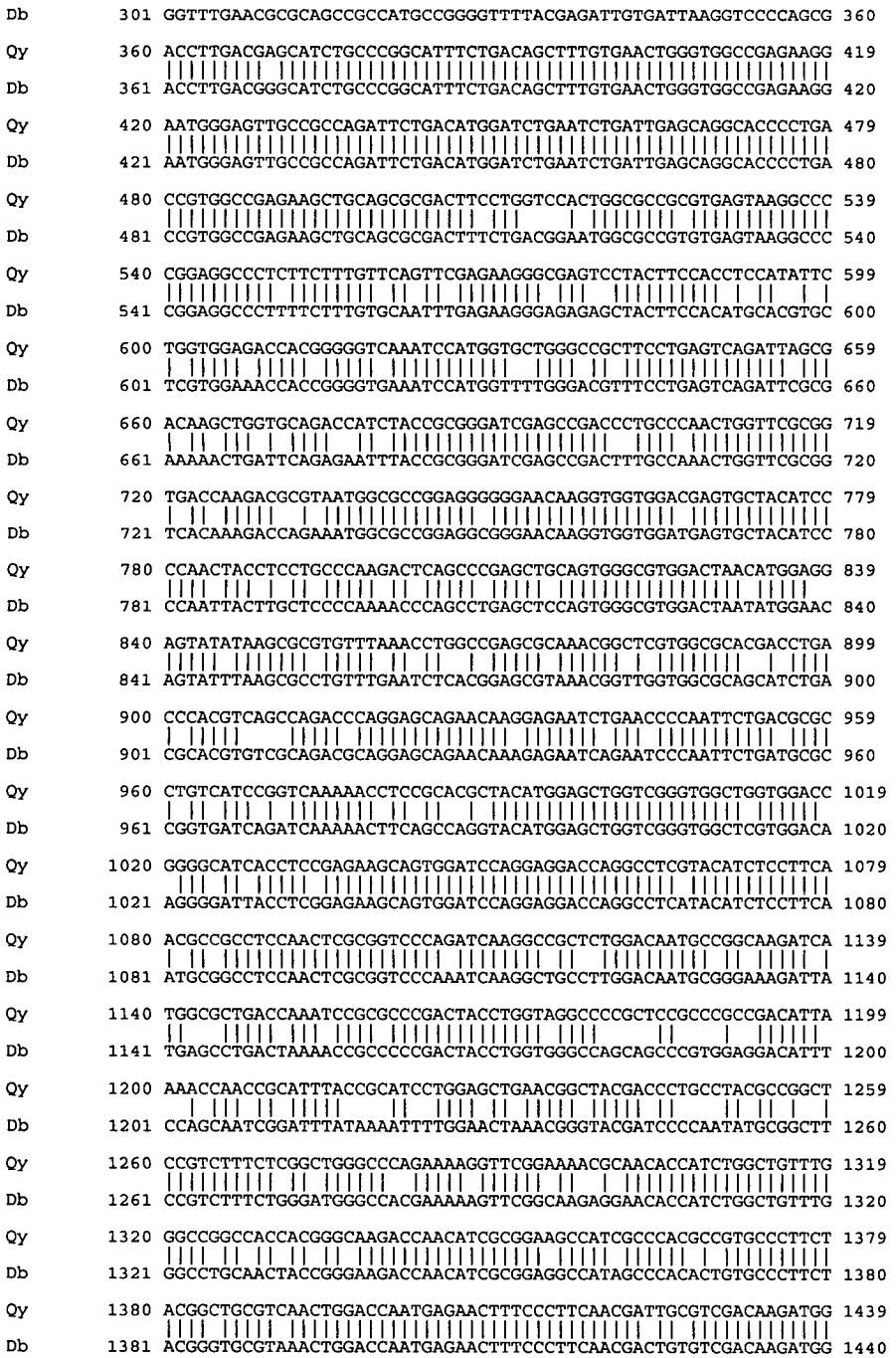
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Qy 1200 AAACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCT 1259
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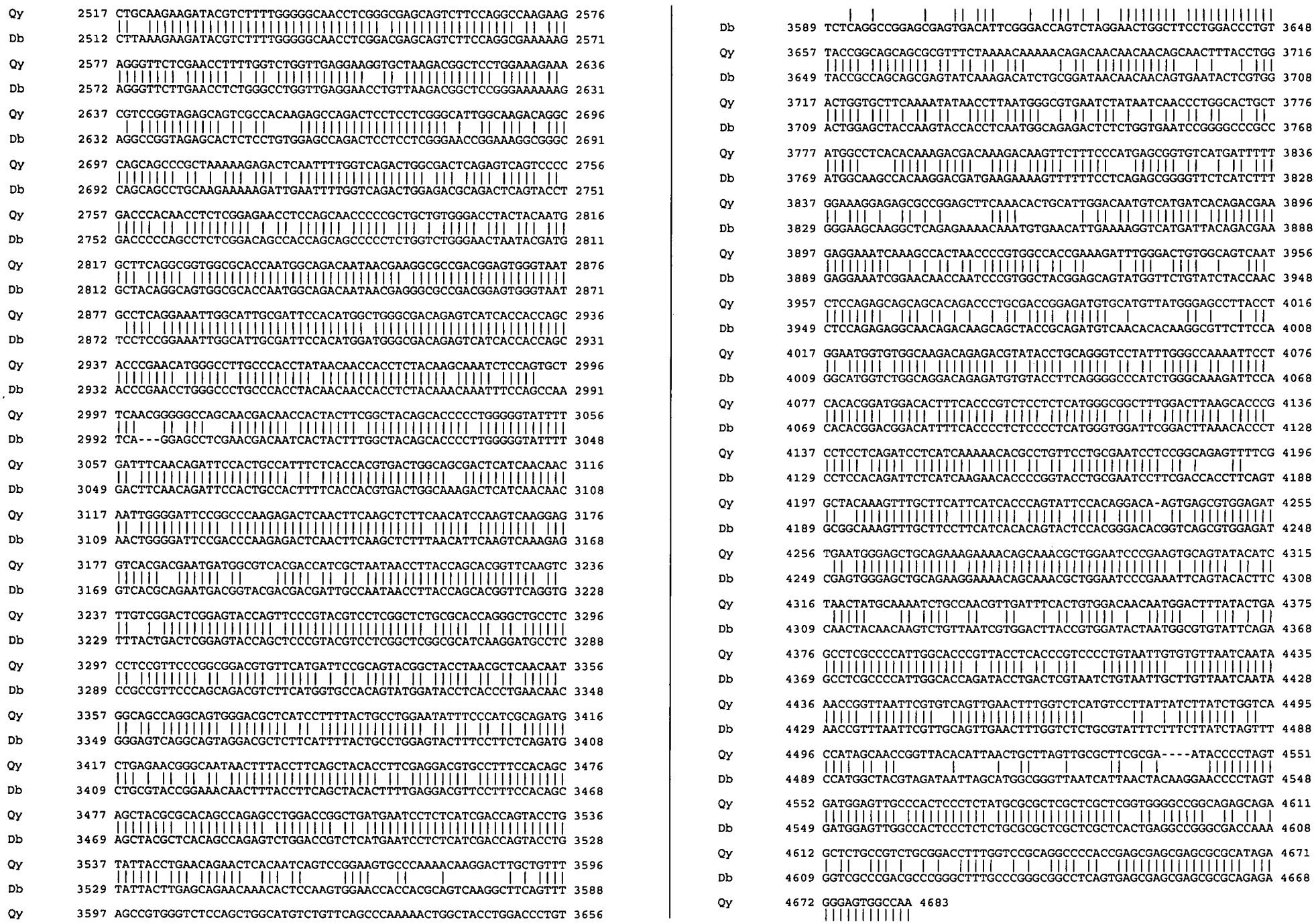
Db 2452 GACAGCGGAGACAACCCGTACCTCAAGTACAACCACGCCGACGCGGAGTTTCAGGAGCGC 2511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Db 2512 CTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGCAGTCTTCCAGGCGAAAAAG 2571
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Db 2572 AGGGTTCTTGAACCTCTGGGCCTGGTTGAGGAACCTGTTAAGACGGCTCCGGGAAAAAAG 2631
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Qy 3477 AGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTG 3536
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Qy 3957 CTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCT 4016
Db 3949 CTCCAGAGAGGCAACAGACAAGCAGCTACCGCAGATGTCAACACACAAGGCGTTCTTCCA 4008
Qy 4017 GGAATGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCT 4076
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Db 4309 CAACTACAACAAGTCTGTTAATCGTGGACTTACCGTGGATACTAATGGCGTGTATTCAGA 4368
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RESULT 7
US-08-475-391-1
; Sequence 1, Application US/08475391
; Patent No. 5786211
;  GENERAL INFORMATION:
;    APPLICANT:  Johnson, Philip R.
;    TITLE OF INVENTION:  Adeno-Associated Virus Materials and
;    TITLE OF INVENTION:  Methods
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 S. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,391
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/254,358
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5786211and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31975
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4680 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-475-391-1

  Query Match             69.8%;  Score 3270.8;  DB 2;  Length 4680;
  Best Local Similarity   82.2%;  Pred. No. 0;
  Matches 3859;  Conservative    0;  Mismatches  812;  Indels   21;  Gaps    8;

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Qy        780 CCAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGG 839
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Db        781 CCAATTACTTGCTCCCCAAAACCCAGCCTGAGCTCCAGTGGGCGTGGACTAATATGGAAC 840

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Qy        960 CTGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACC 1019
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Qy       1080 ACGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCA 1139
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Db       1081 ATGCGGCCTCCAACTCGCGGTCCCAAATCAAGGCTGCCTTGGACAATGCGGGAAAGATTA 1140

Qy       1140 TGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACATTA 1199
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Qy       1200 AAACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCT 1259
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Db       1201 CCAGCAATCGGATTTATAAAATTTTGGAACTAAACGGGTACGATCCCCAATATGCGGCTT 1260

Qy       1260 CCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTTTG 1319
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Qy       1320 GGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCT 1379
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Db       1321 GGCCTGCAACTACCGGGAAGACCAACATCGCGGAGGCCATAGCCCACACTGTGCCCTTCT 1380

Qy       1380 ACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGG 1439
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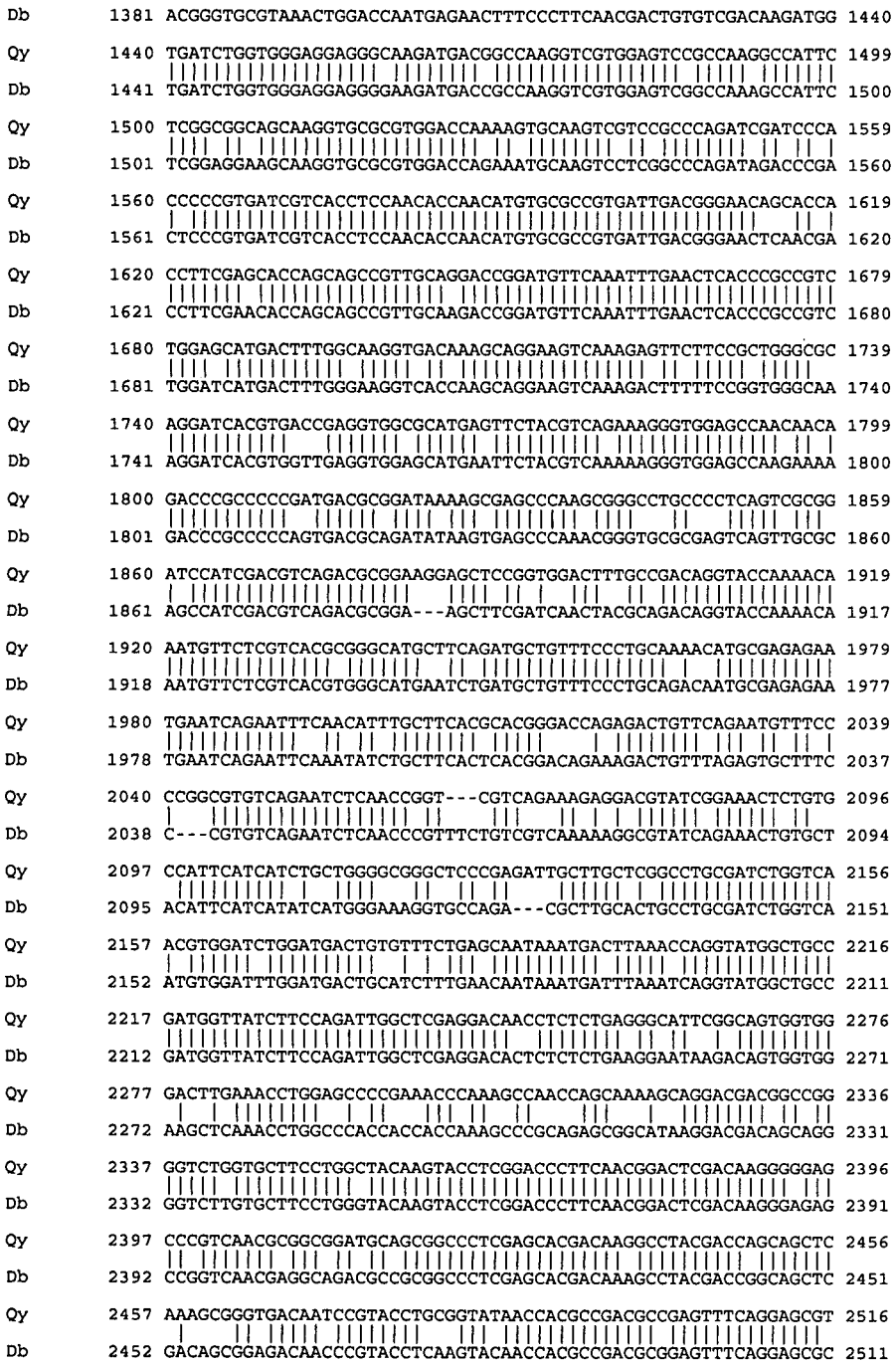
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; Sequence 1, Application US/08709609
; Patent No. 5858775
; GENERAL INFORMATION:
; APPLICANT: Johnson, Philip R.
; TITLE OF INVENTION: Adeno-Associated Virus Materials and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,609
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5858775and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31975
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
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; LENGTH: 4680 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-709-609-1

Query Match 69.8%; Score 3270.8; DB 2; Length 4680;
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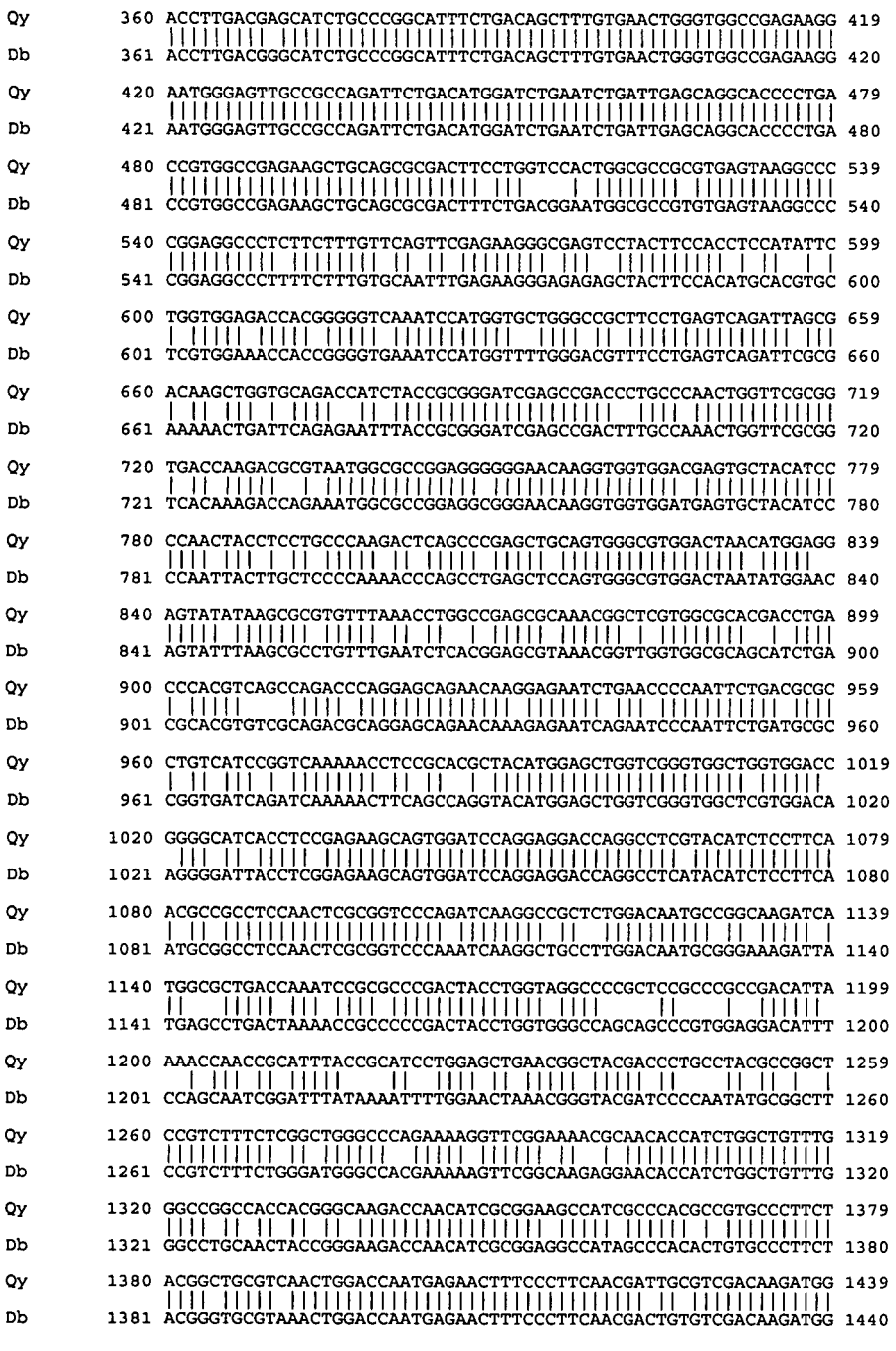
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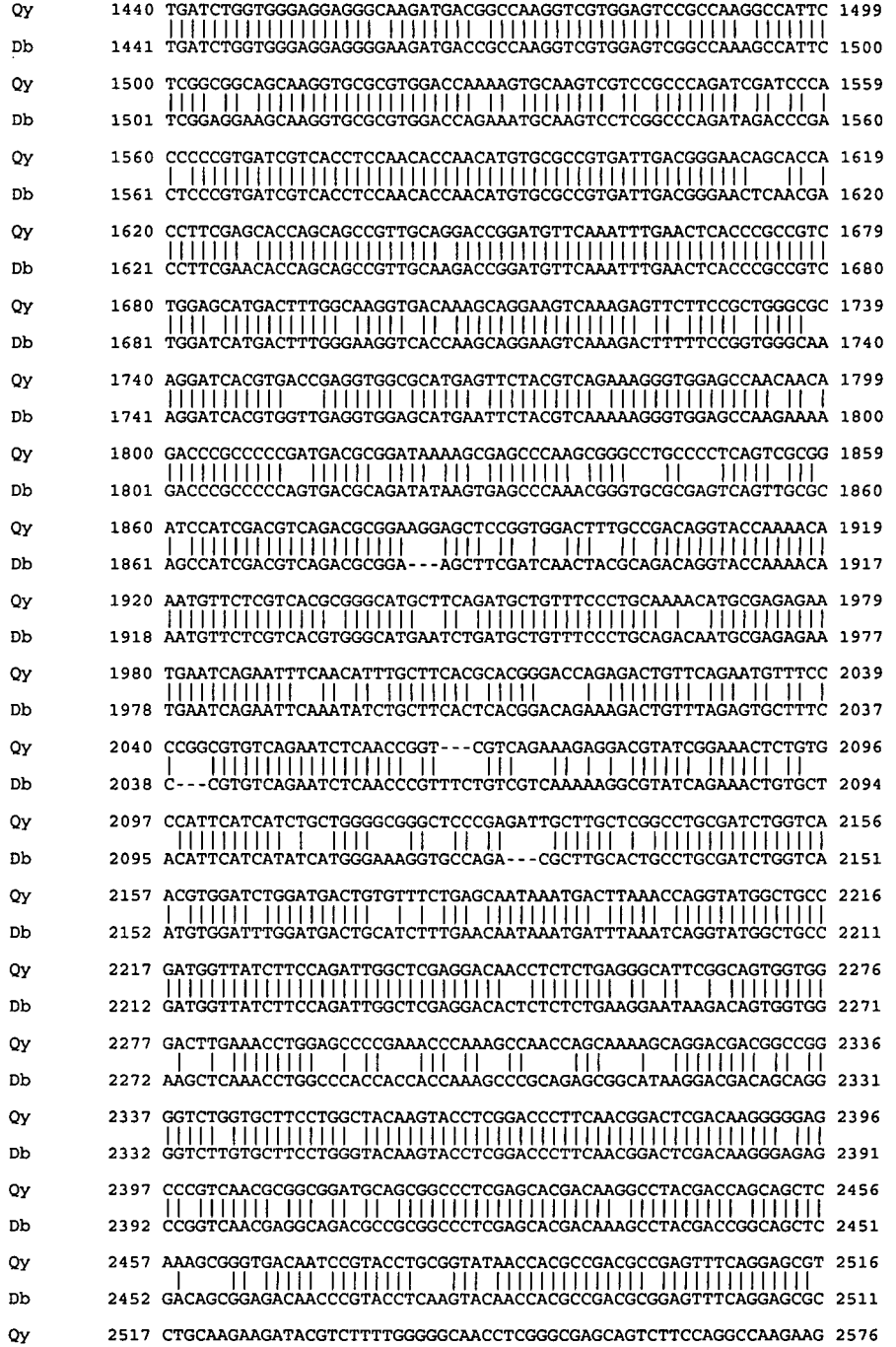
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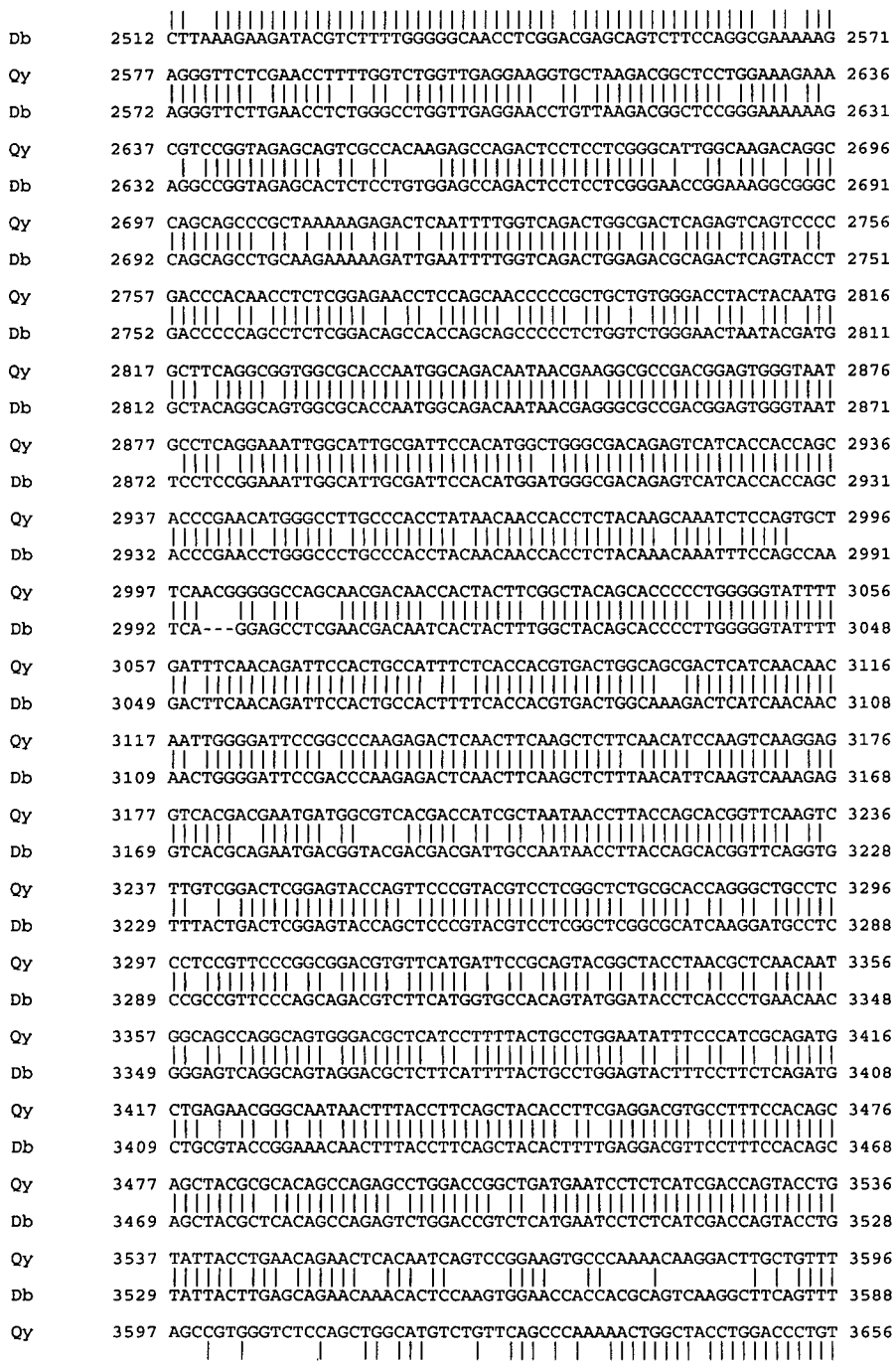
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Qy 2757 GACCCACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATG 2816
Db 2752 GACCCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATG 2811
Qy 2817 GCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAAT 2876
Db 2812 GCTACAGGCAGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGACGGAGTGGGTAAT 2871
Qy 2877 GCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGC 2936
Db 2872 TCCTCCGGAAATTGGCATTGCGATTCCACATGGATGGGCGACAGAGTCATCACCACCAGC 2931
Qy 2937 ACCCGAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCT 2996
Db 2932 ACCCGAACCTGGGCCCTGCCCACCTACAACAACCACCTCTACAAACAAATTTCCAGCCAA 2991
Qy 2997 TCAACGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTT 3056
Db 2992 TCA---GGAGCCTCGAACGACAATCACTACTTTGGCTACAGCACCCCTTGGGGGTATTTT 3048
Qy 3057 GATTTCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAAC 3116
Db 3049 GACTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAAAGACTCATCAACAAC 3108
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Db 3169 GTCACGCAGAATGACGGTACGACGACGATTGCCAATAACCTTACCAGCACGGTTCAGGTG 3228
Qy 3237 TTGTCGGACTCGGAGTACCAGTTCCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTC 3296
Db 3229 TTTACTGACTCGGAGTACCAGCTCCCGTACGTCCTCGGCTCGGCGCATCAAGGATGCCTC 3288
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Qy 3357 GGCAGCCAGGCAGTGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATG 3416
Db 3349 GGGAGTCAGGCAGTAGGACGCTCTTCATTTTACTGCCTGGAGTACTTTCCTTCTCAGATG 3408
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Qy 3597 AGCCGTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGT 3656
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Qy 3657 TACCGGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGG 3716
Db 3649 TACCGCCAGCAGCGAGTATCAAAGACATCTGCGGATAACAACAACAGTGAATACTCGTGG 3708
Qy 3717 ACTGGTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCT 3776
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Qy 3957 CTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCT 4016
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Qy 4077 CACACGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCG 4136
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Db 4369 GCCTCGCCCCATTGGCACCAGATACCTGACTCGTAATCTGTAATTGCTTGTTAATCAATA 4428
Qy 4436 AACCGGTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCA 4495
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Db 4489 CCATGGCTACGTAGATAATTAGCATGGCGGGTTAATCATTAACTACAAGGAACCCCTAGT 4548
Qy 4552 GATGGAGTTGCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGA 4611
Db 4549 GATGGAGTTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAA 4608
Qy 4612 GCTCTGCCGTCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGA 4671
Db 4609 GGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGA 4668
Qy 4672 GGGAGTGGCCAA 4683
Db 4669 GGGAGTGGCCAA 4680

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RESULT 9
PCT-US95-07178-1
; Sequence 1, Application PC/TUS9507178
;  GENERAL INFORMATION:
;    APPLICANT:  Johnson, Philip R.
;    TITLE OF INVENTION:  Adeno-Associated Virus Materials and
;    TITLE OF INVENTION:  Methods
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 S. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/07178
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Noland, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31975
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4680 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US95-07178-1

  Query Match             69.8%;  Score 3270.8;  DB 7;  Length 4680;
  Best Local Similarity   82.2%;  Pred. No. 0;
  Matches 3859;  Conservative    0;  Mismatches  812;  Indels   21;  Gaps    8;

Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
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Db          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
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Qy        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180
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Qy        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240
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Qy        241 GTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGA 300
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Qy        301 GGTTTGAACGCGCAG-CGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCG 359
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Qy        360 ACCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGG 419
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Db        361 ACCTTGACGGGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGG 420

Qy        420 AATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGA 479
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Qy        480 CCGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCGCCGCGTGAGTAAGGCCC 539
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Db        481 CCGTGGCCGAGAAGCTGCAGCGCGACTTTCTGACGGAATGGCGCCGTGTGAGTAAGGCCC 540

Qy        540 CGGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTACTTCCACCTCCATATTC 599
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Db        541 CGGAGGCCCTTTTCTTTGTGCAATTTGAGAAGGGAGAGAGCTACTTCCACATGCACGTGC 600

Qy        600 TGGTGGAGACCACGGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGCG 659
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Qy        660 ACAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCTGCCCAACTGGTTCGCGG 719
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Qy        720 TGACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCC 779
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Qy        780 CCAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGG 839
              |||| ||| | || ||||| || ||||| ||||| |||||||||||||||| |||||
Db        781 CCAATTACTTGCTCCCCAAAACCCAGCCTGAGCTCCAGTGGGCGTGGACTAATATGGAAC 840

Qy        840 AGTATATAAGCGCGTGTTTAAACCTGGCCGAGCGCAAACGGCTCGTGGCGCACGACCTGA 899
              ||||| ||||||| |||| || ||  | ||||| |||||  | ||||||||  | ||||
Db        841 AGTATTTAAGCGCCTGTTTGAATCTCACGGAGCGTAAACGGTTGGTGGCGCAGCATCTGA 900

Qy        900 CCCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGC 959
              | ||||||    ||||| |||||||||||||| ||||||| ||| ||||||||||| ||||
Db        901 CGCACGTGTCGCAGACGCAGGAGCAGAACAAAGAGAATCAGAATCCCAATTCTGATGCGC 960

Qy        960 CTGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACC 1019
              | || ||| | |||||||| || ||  | ||||||||||||||||||||| ||||||
Db        961 CGGTGATCAGATCAAAAACTTCAGCCAGGTACATGGAGCTGGTCGGGTGGCTCGTGGACA 1020

Qy       1020 GGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCA 1079
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Db       1021 AGGGGATTACCTCGGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCATACATCTCCTTCA 1080

Qy       1080 ACGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCA 1139
              | || |||||||||||||||||||| |||||||| ||  |||||||||| || ||||| |
Db       1081 ATGCGGCCTCCAACTCGCGGTCCCAAATCAAGGCTGCCTTGGACAATGCGGGAAAGATTA 1140

Qy       1140 TGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACATTA 1199
              ||   ||||| ||| |||| |||||||||||||| ||||     ||     | ||||||
Db       1141 TGAGCCTGACTAAAACCGCCCCCGACTACCTGGTGGGCCAGCAGCCCGTGGAGGACATTT 1200

Qy       1200 AAACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCT 1259
                | ||| || |||||     ||  |||| || ||||| ||||| ||    || || | |
Db       1201 CCAGCAATCGGATTTATAAAATTTTGGAACTAAACGGGTACGATCCCCAATATGCGGCTT 1260

Qy       1260 CCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTTTG 1319
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Db       1261 CCGTCTTTCTGGGATGGGCCACGAAAAAGTTCGGCAAGAGGAACACCATCTGGCTGTTTG 1320

Qy       1320 GGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCT 1379
              |||| || || || || |||||||||||||||||| ||||| ||||||  | ||||||||||
Db       1321 GGCCTGCAACTACCGGGAAGACCAACATCGCGGAGGCCATAGCCCACACTGTGCCCTTCT 1380

Qy       1380 ACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGG 1439
              |||| ||||| |||||||||||||||||||||||||||||||||||| || ||||||||||
Db       1381 ACGGGTGCGTAAACTGGACCAATGAGAACTTTCCCTTCAACGACTGTGTCGACAAGATGG 1440

Qy       1440 TGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTC 1499
              |||||||||||||||||| |||||||| |||||||||||||||| ||||| |||||||
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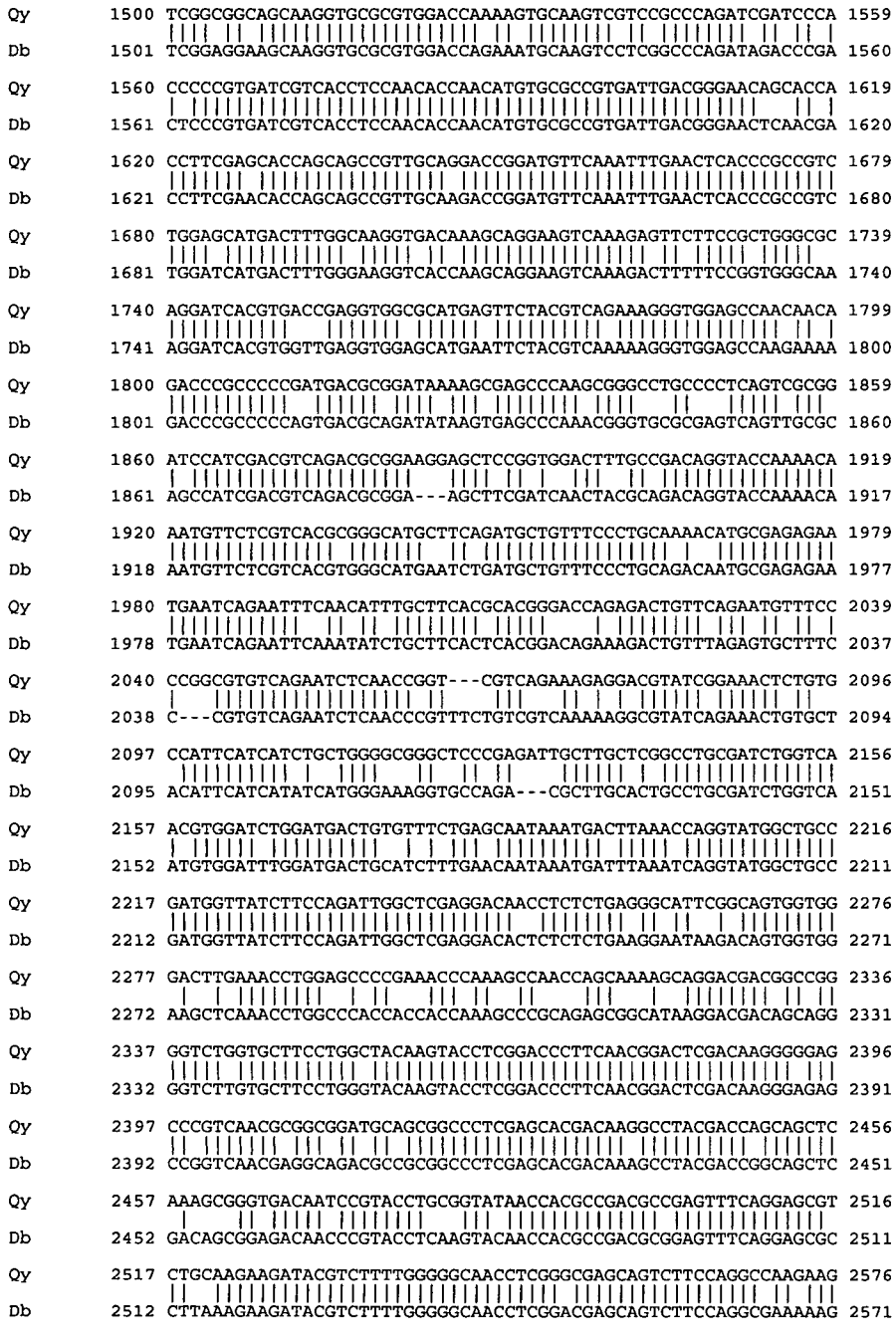

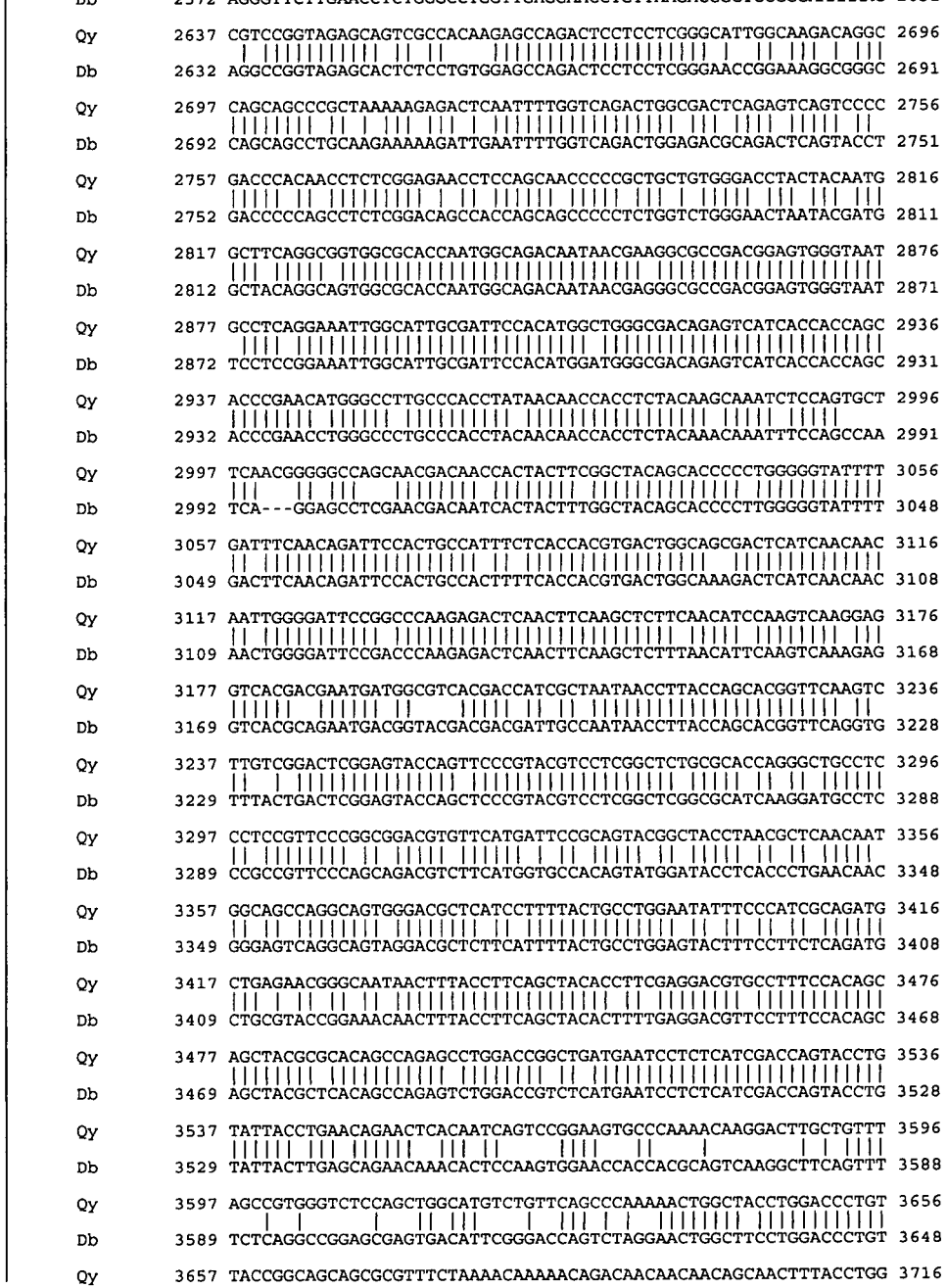

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Qy       3717 ACTGGTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCT 3776

Db       3709 ACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGGCCCGCC 3768

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Db       3769 ATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTTTCCTCAGAGCGGGGTTCTCATCTTT 3828

Qy       3837 GGAAAGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAA 3896

Db       3829 GGGAAGCAAGGCTCAGAGAAAACAAATGTGAACATTGAAAAGGTCATGATTACAGACGAA 3888

Qy       3897 GAGGAAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAAT 3956

Db       3889 GAGGAAATCGGAACAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAAC 3948

Qy       3957 CTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCT 4016

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Db       4009 GGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGCCCATCTGGGCAAAGATTCCA 4068

Qy       4077 CACACGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCG 4136

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Db       4609 GGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGA 4668

Qy       4672 GGGAGTGGCCAA 4683

Db       4669 GGGAGTGGCCAA 4680

RESULT 10
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US-09-807-802A-18
; Sequence 18, Application US/09807802A
; Patent No. 6759237
; GENERAL INFORMATION:
;  APPLICANT: Wilson, James M.
;  APPLICANT:  Xiao, Weidong
;  TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
;  TITLE OF INVENTION:  Vectors and Host Cells Containing Same
;  FILE REFERENCE: GNVPN.031USA
;  CURRENT APPLICATION NUMBER: US/09/807,802A
;  CURRENT FILING DATE:  2002-02-21
;  PRIOR APPLICATION NUMBER: US 60/107,114
;  PRIOR FILING DATE: 1998-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/25694
;  PRIOR FILING DATE: 1999-11-02
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 4681
;   TYPE: DNA
;   ORGANISM: AAV-2
US-09-807-802A-18

  Query Match            69.8%;  Score 3267.8;  DB 3;  Length 4681;
  Best Local Similarity   82.3%;  Pred. No. 0;
  Matches 3864;  Conservative    0;  Mismatches  807;  Indels   22;  Gaps    9;

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Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120

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Db        361 ACCTTGACGGGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGG 420

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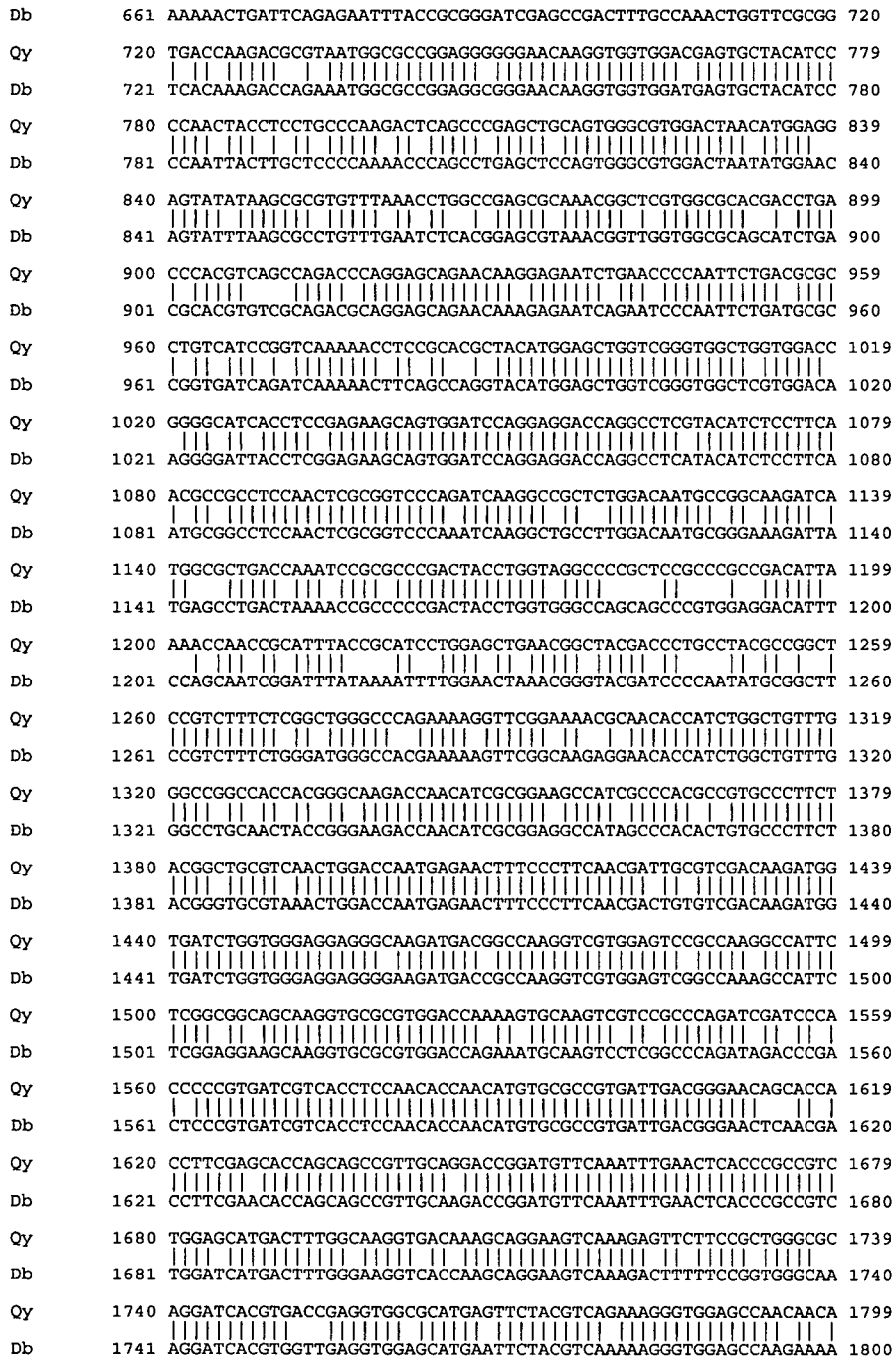
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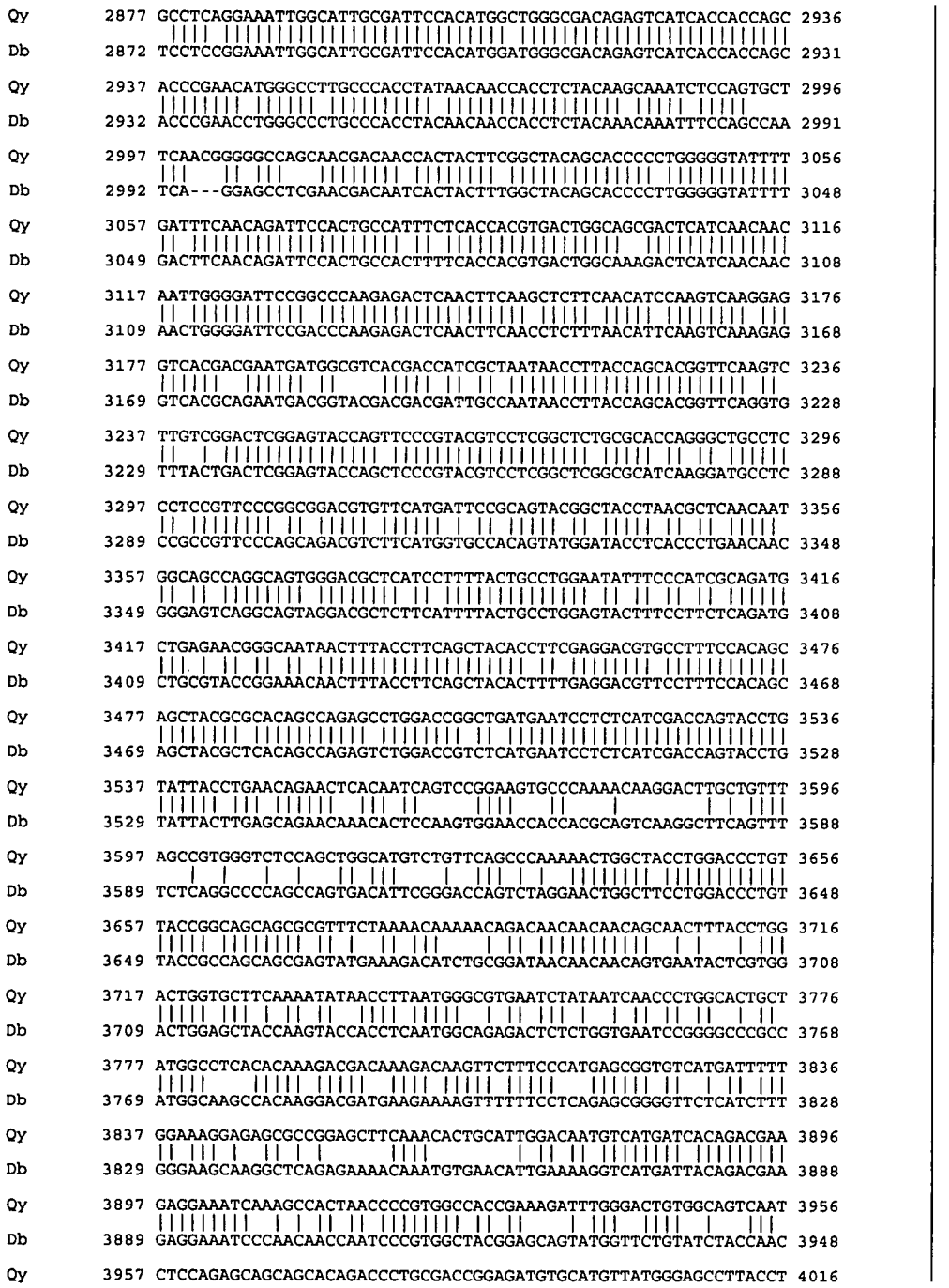

RESULT 11
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; Sequence 1, Application US/09782378A
; Patent No. 6916635
; GENERAL INFORMATION:
; APPLICANT: Hearing, Patrick
; APPLICANT: Bahou, Wadie
; APPLICANT: Sandalon, Ziv
; APPLICANT: Gnatenko, Dmitri
; TITLE OF INVENTION: Adenoviral Vectors
; FILE REFERENCE: STONYB-04970
; CURRENT APPLICATION NUMBER: US/09/782,378A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/237,747
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 27
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; TYPE: DNA
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Query Match 69.3%; Score 3244.2; DB 3; Length 4675;
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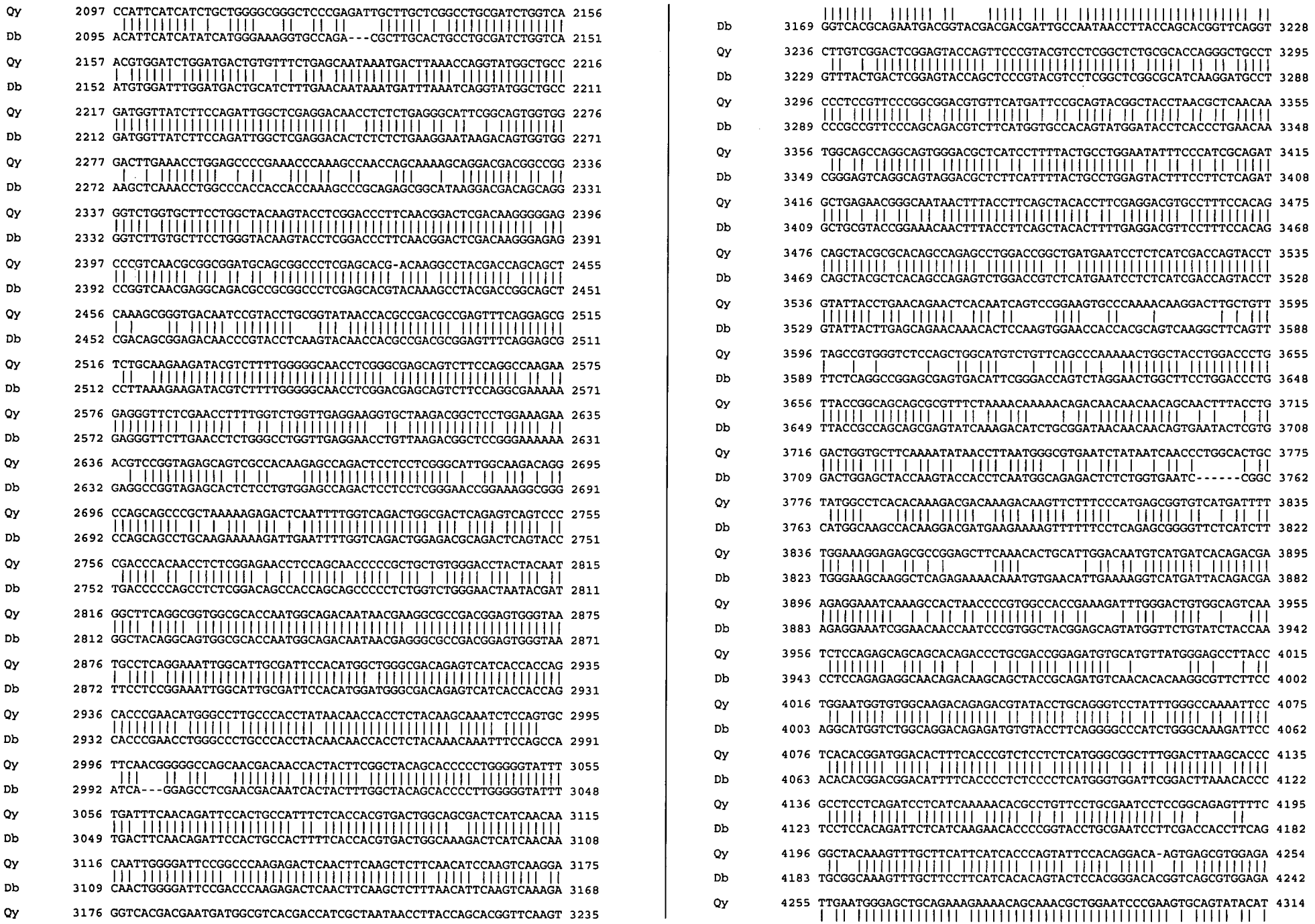

RESULT 12
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; Sequence 2, Application US/09782378A
; Patent No. 6916635
; GENERAL INFORMATION:
; APPLICANT: Hearing, Patrick
; APPLICANT: Bahou, Wadie
; APPLICANT: Sandalon, Ziv
; APPLICANT: Gnatenko, Dmitri
; TITLE OF INVENTION: Adenoviral Vectors
; FILE REFERENCE: STONYB-04970
; CURRENT APPLICATION NUMBER: US/09/782,378A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/237,747
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 4675
; TYPE: DNA
; ORGANISM: Human adeno-associated virus 2
US-09-782-378A-2

Query Match 69.3%; Score 3244.2; DB 3; Length 4675;
Best Local Similarity 82.2%; Pred. No. 0;
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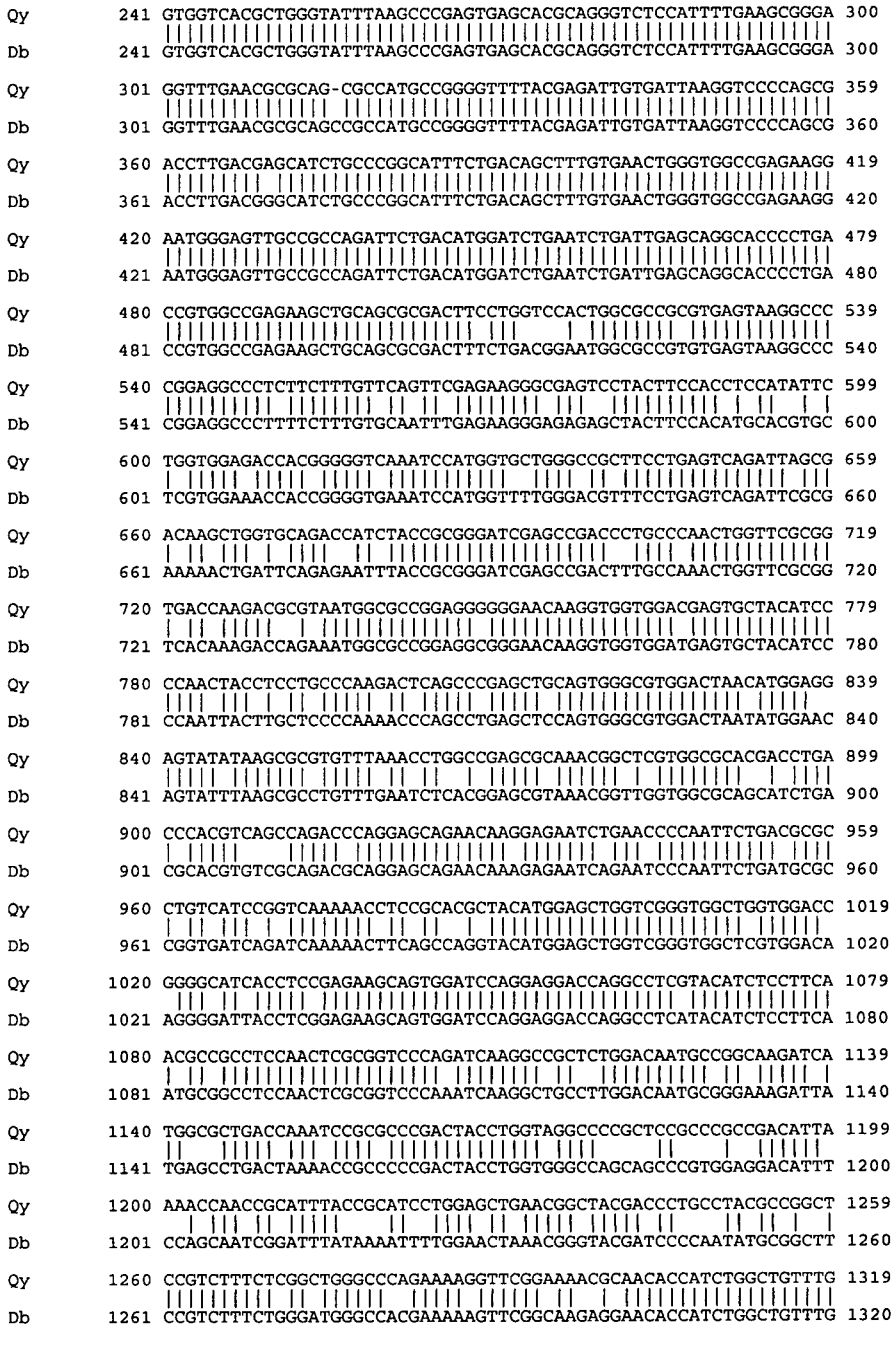

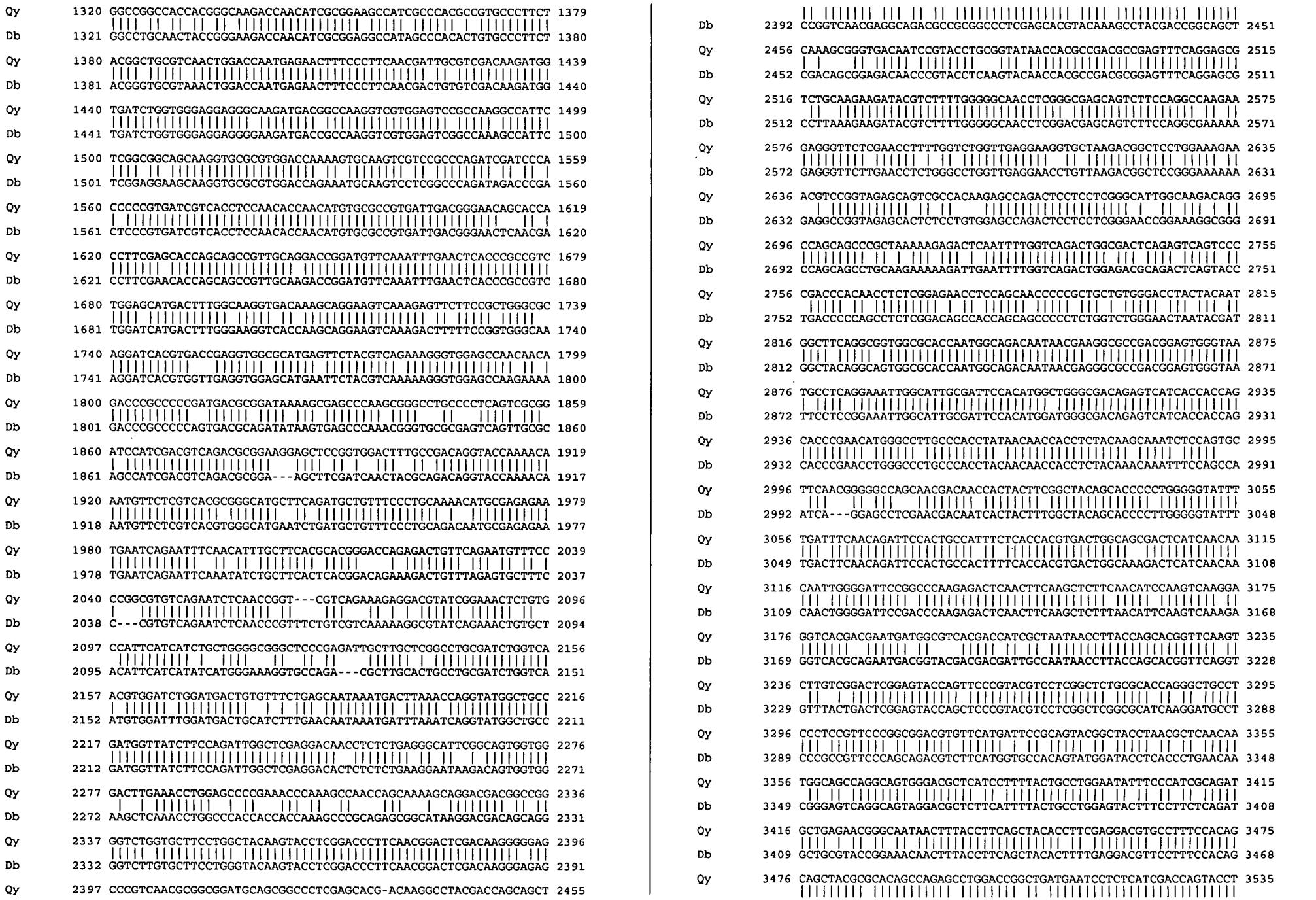

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Db       4003 AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGCCCATCTGGGCAAAGATTCC 4062

Qy       4076 TCACACGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCC 4135

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Qy       4136 GCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTC 4195

Db       4123 TCCTCCACAGATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCACCTTCAG 4182

Qy       4196 GGCTACAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACA-AGTGAGCGTGGAGA 4254

Db       4183 TGCGGCAAAGTTTGCTTCCTTCATCACACAGTACTCCACGGGACACGGTCAGCGTGGAGA 4242

Qy       4255 TTGAATGGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACAT 4314

Db       4243 TCGAGTGGGAGCTGCAGAAGGAAAACAGCAAACGCTGGAATCCCGAAATTCAGTACACTT 4302

Qy       4315 CTAACTATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTG 4374

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Db       4603 AGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAG 4662

Qy       4671 AGGGAGTGGCCAA 4683

Db       4663 AGGGAGTGGCCAA 4675
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RESULT 13
US-10-111-708-1
; Sequence 1, Application US/10111708
; Patent No. 6995010
; GENERAL INFORMATION:
; APPLICANT: UENO, Takashi
; APPLICANT: MATSUMURA, Hajime
; APPLICANT: TANAKA, Keiji
; APPLICANT: IWASAKI, Tomoko
; APPLICANT: UENO, Mitsuhiro
; APPLICANT: FUJINAGA, Kei
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: GENE TRANSFER METHOD
; FILE REFERENCE: UENO=9
; CURRENT APPLICATION NUMBER: US/10/111,708
; CURRENT FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: PCT JP00 07373
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: JP 11/308839
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4675
; TYPE: DNA
; ORGANISM: Adeno-associated Virus
US-10-111-708-1

Query Match 69.3%; Score 3244.2; DB 4; Length 4675;
Best Local Similarity 82.2%; Pred. No. 0;
Matches 3857; Conservative 0; Mismatches 808; Indels 28; Gaps 10;

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Db          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60

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Qy        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180

Db        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180

Qy        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240

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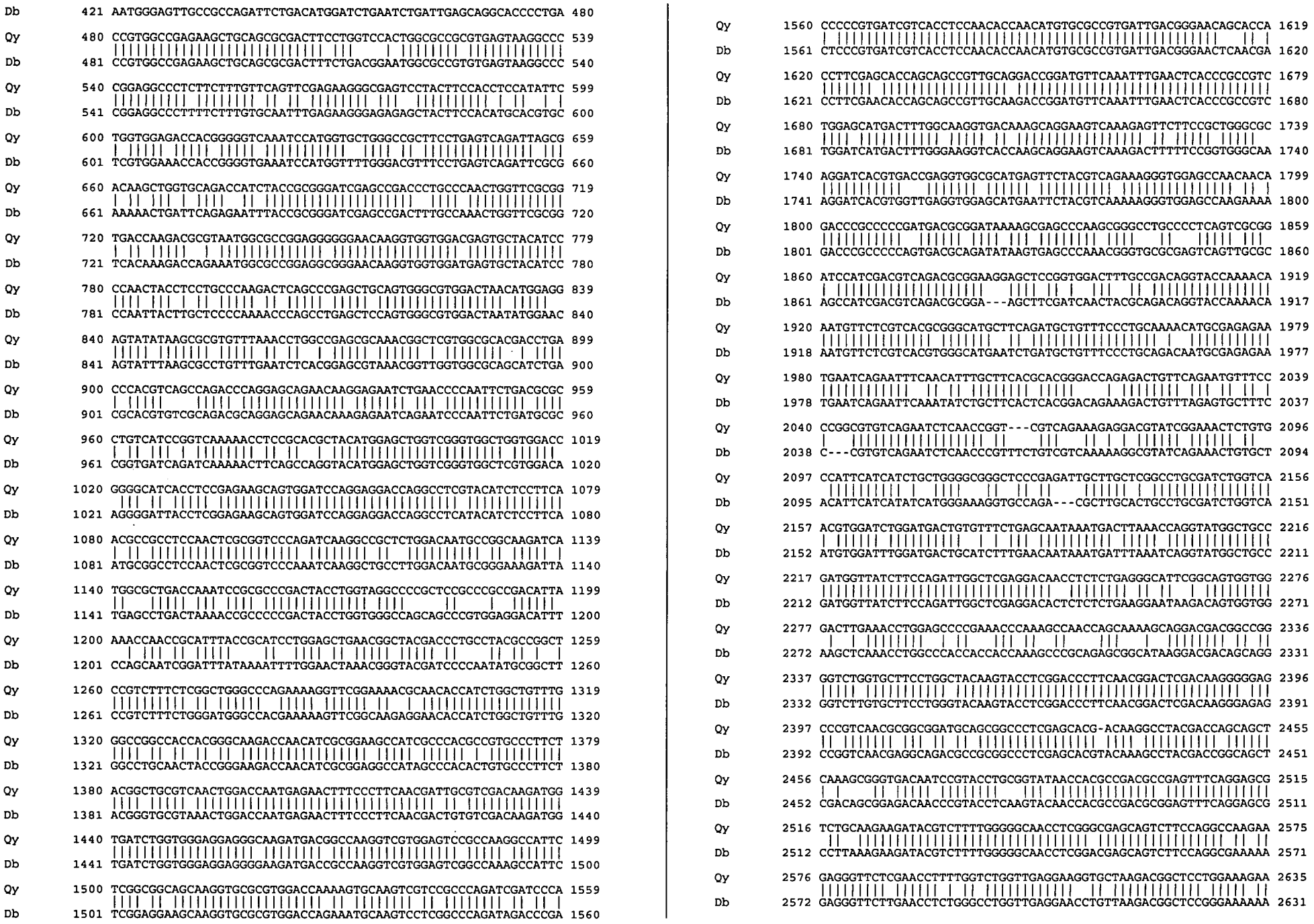

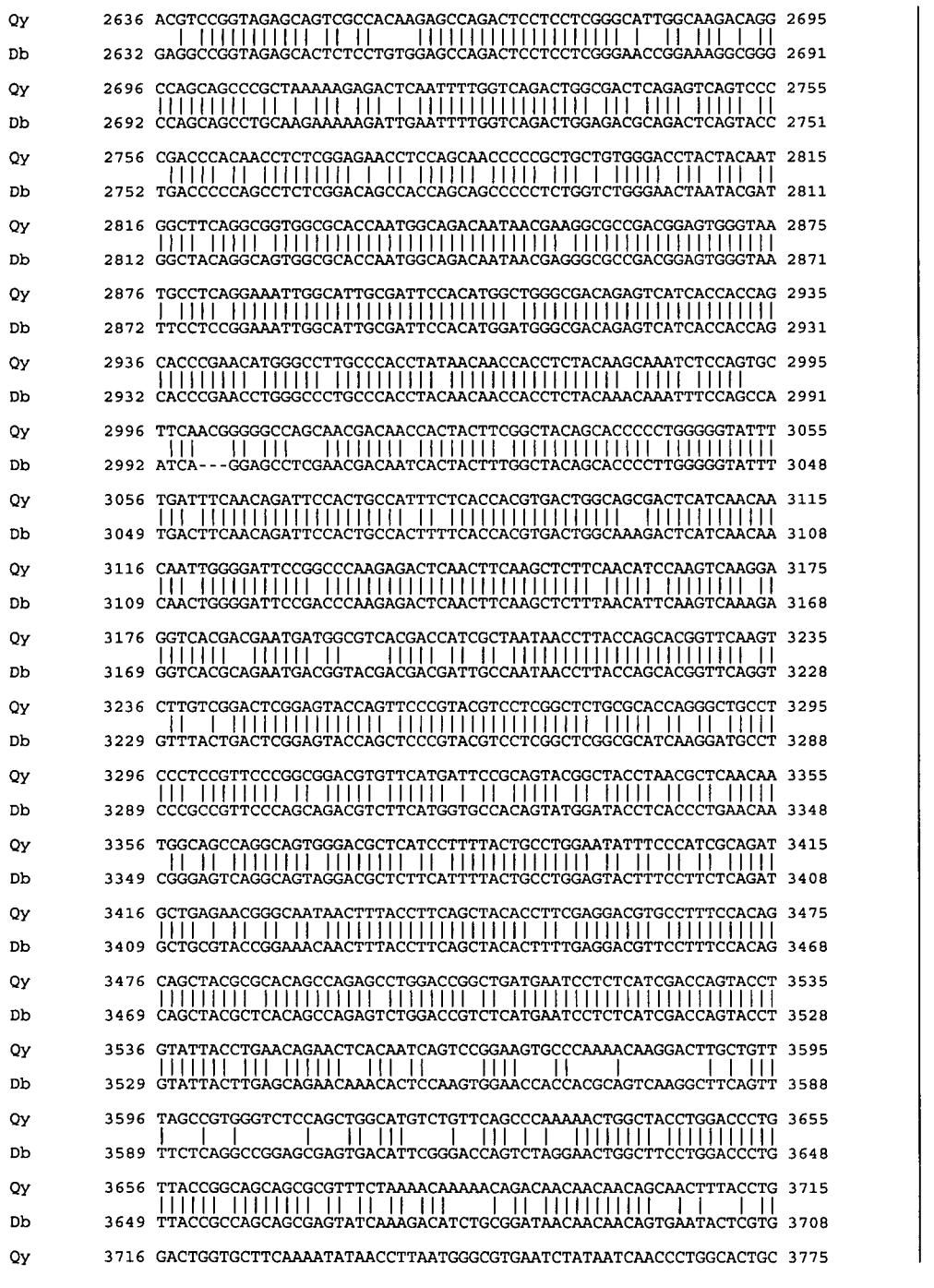

RESULT 14
US-09-770-315-3
; Sequence 3, Application US/09770315
; Patent No. 6429001
; GENERAL INFORMATION:

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;  APPLICANT: Chiron Corporation
;  TITLE OF INVENTION: Recombinant AAV Packaging Systems
;  FILE REFERENCE: 20263-501
;  CURRENT APPLICATION NUMBER: US/09/770,315
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 60/178,536
;  PRIOR FILING DATE: 2000-01-26
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 7557
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: recombinant DNA
US-09-770-315-3

  Query Match             66.5%;  Score 3114.4;  DB 3;  Length 7557;
  Best Local Similarity   81.7%;  Pred. No. 0;
  Matches 3705;  Conservative    0;  Mismatches  771;  Indels   58;  Gaps    7;

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Db          4 GCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCAAAGCCCGGGCGTCGGGCGACCTTTGG 63

Qy         78 CCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAG 137
Db         64 TCGCCCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTGA 123

Qy        138 GGG-------------------------------------------TTCCTGGAGGGGTGG 155
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Qy        156 AGTCGTGACGTGAATTACGTCATAGGGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGT 215
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Qy        216 GTTTTGCGACATTTTGCGACACCATGTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCAC 275
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Db        604 GAGAGCTACTTCCACATGCACGTGCTCGTGGAAACCACCGGGGTGAAATCCATGGTTTTG 663

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Db        664 GGACGTTTCCTGAGTCAGATTCGCGAAAAACTGATTCAGAGAATTTACCGCGGGATCGAG 723

Qy        695 CCGACCCTGCCCAACTGGTTCGCGGTGACCAAGACGCGTAATGGCGCCGGAGGGGGGAAC 754
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Qy        875 AAACGGCTCGTGGCGCACGACCTGACCCACGTCAGCCAGACCCAGGAGCAGAACAAGGAG 934
Db        904 AAACGGTTGGTGGCGCAGCATCTGACGCACGTGTCGCAGACGCAGGAGCAGAACAAAGAG 963

Qy        935 AATCTGAACCCCAATTCTGACGCGCCTGTCATCCGGTCAAAAACCTCCGCACGCTACATG 994
Db        964 AATCAGAATCCCAATTCTGATGCGCCGGTGATCAGATCAAAAACTTCAGCCAGGTACATG 1023

Qy        995 GAGCTGGTCGGGTGGCTGGTGGACCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAG 1054
Db       1024 GAGCTGGTCGGGTGGCTCGTGGACAAGGGGATTACCTCGGAGAAGCAGTGGATCCAGGAG 1083

Qy       1055 GACCAGGCCTCGTACATCTCCTTCAACGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCC 1114
Db       1084 GACCAGGCCTCATACATCTCCTTCAATGCGGCCTCCAACTCGCGGTCCCAAATCAAGGCT 1143

Qy       1115 GCTCTGGACAATGCCGGCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTA 1174
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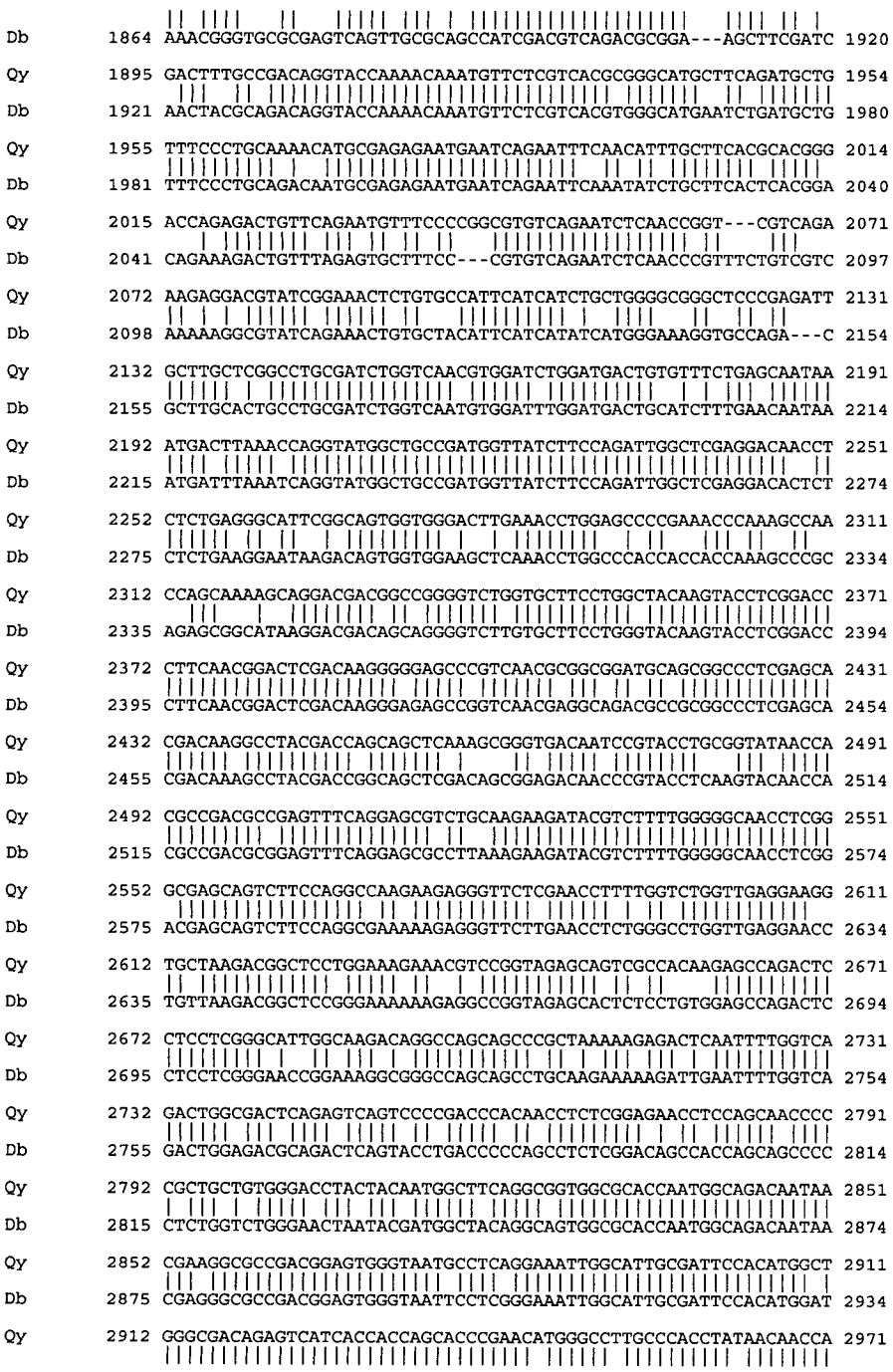
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Qy 3692 CAACAACAACAGCAACTTTACCTGGACTGGTGCTTCAAAATATAACCTTAATGGGCGTGA 3751
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RESULT 15
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; Sequence 5, Application US/09438268
; Patent No. 6491907
; GENERAL INFORMATION:
;  APPLICANT: Rabinowitz, Joseph E.
;  APPLICANT: Samulski, Richard J
;  APPLICANT: Xiao, Weidong
;  TITLE OF INVENTION: VIRUS VECTORS AND METHOD OF MAKING AND ADMINISTERING
;  TITLE OF INVENTION: THE SAME
;  FILE REFERENCE: 5470-186
;  CURRENT APPLICATION NUMBER: US/09/438,268
;  CURRENT FILING DATE: 1999-11-10
;  EARLIER APPLICATION NUMBER: 60/107,840
;  EARLIER FILING DATE: 1998-11-10
;  EARLIER APPLICATION NUMBER: 60/123,651
;  EARLIER FILING DATE: 1999-03-10
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 8179
;   TYPE: DNA
;   ORGANISM: Virus
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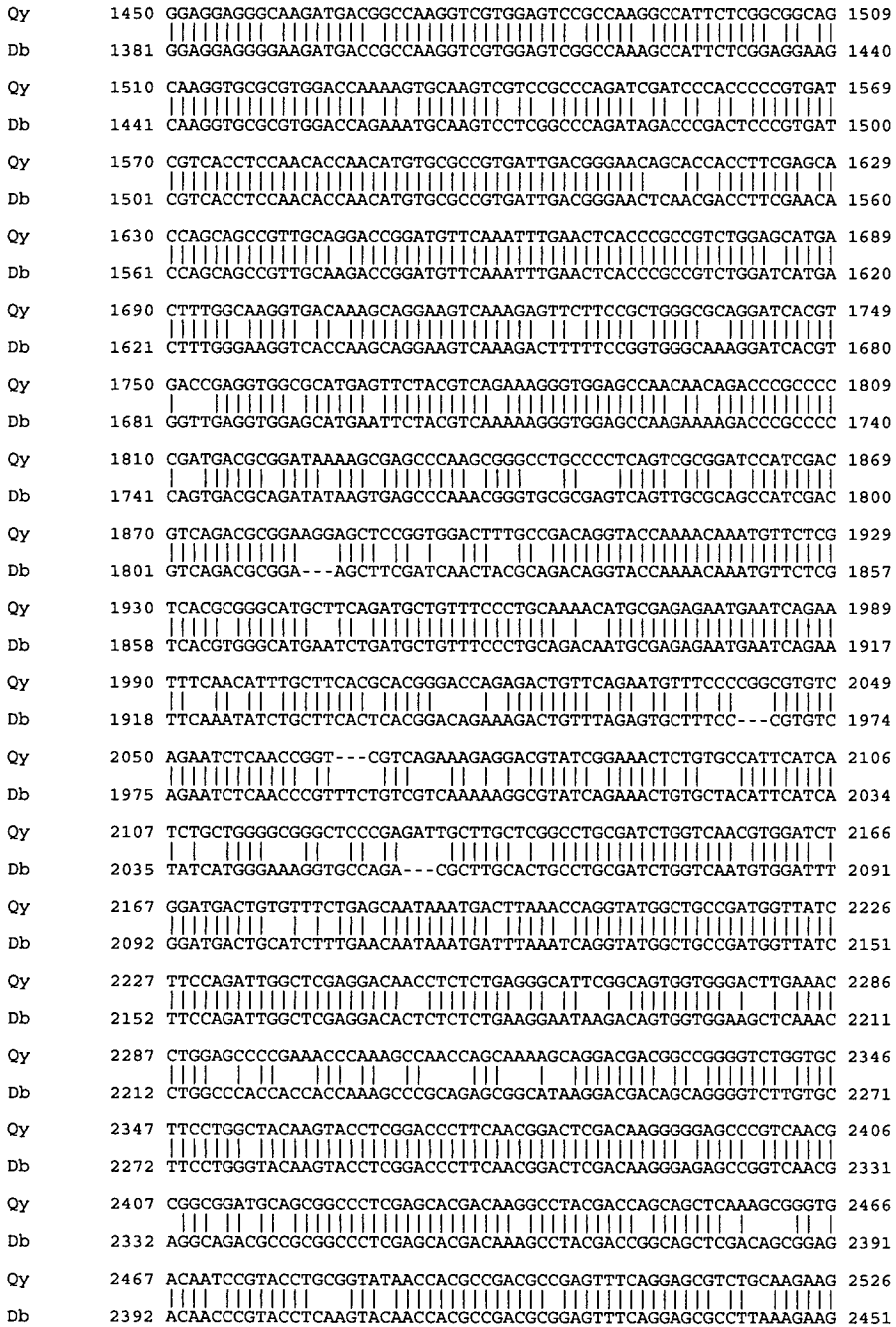

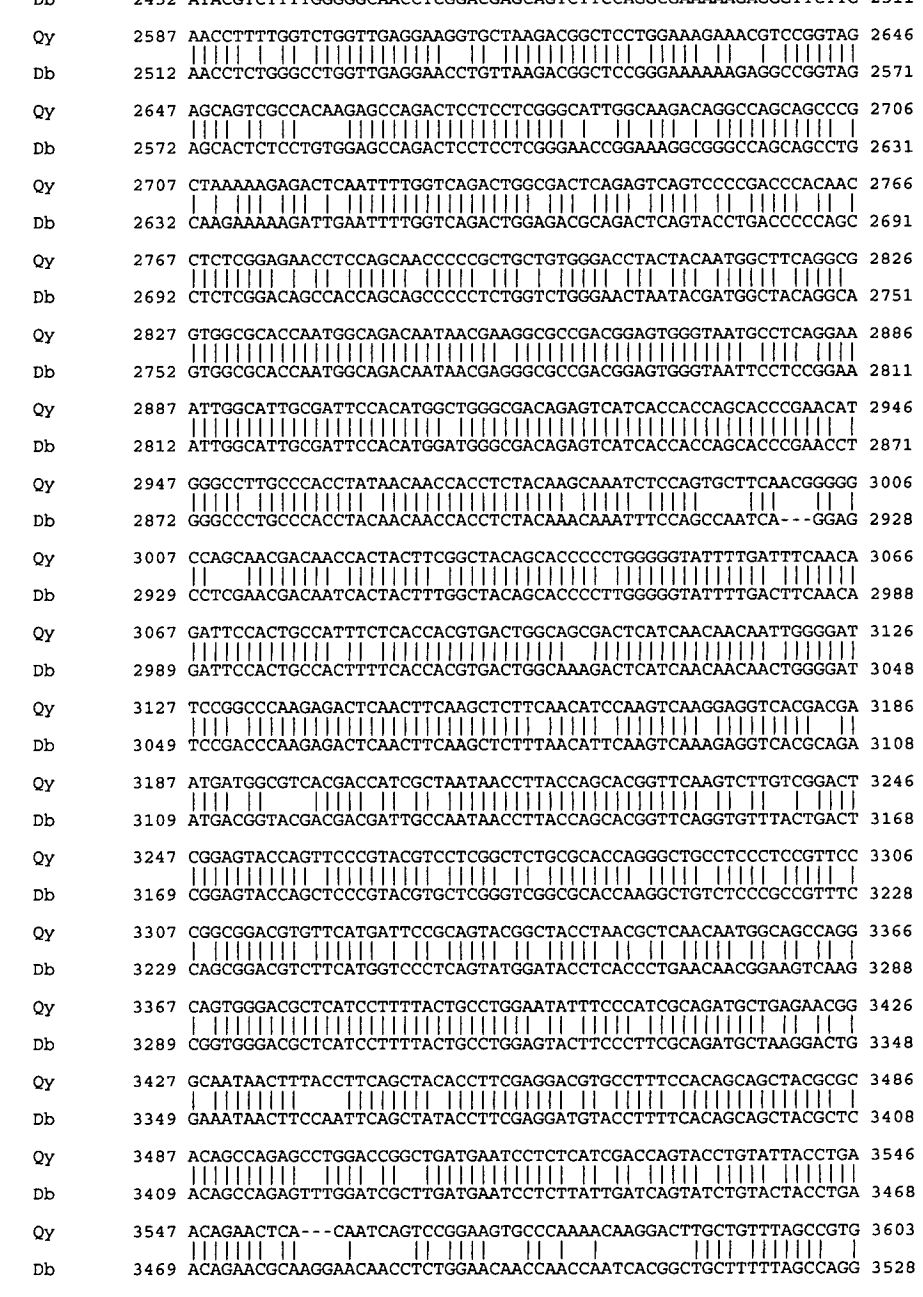

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Sequence 1, Application US/11327357
; Publication No. US20060105983A1
; GENERAL INFORMATION:
; APPLICANT: BTG International Ltd
; APPLICANT: BEARD DR, PETER
; APPLICANT: RAJ DR, KENNETH
; TITLE OF INVENTION: CYTOTOXIC AGENTS
; FILE REFERENCE: 142184WO
; CURRENT APPLICATION NUMBER: US/11/327,357
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: 0009887.1
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4675
; TYPE: DNA
; ORGANISM: adeno-associated virus 2
US-11-327-357-1

Query Match 69.3%; Score 3244.2; DB 7; Length 4675;
Best Local Similarity 82.2%; Pred. No. 0;
Matches 3857; Conservative 0; Mismatches 808; Indels 28; Gaps 10;

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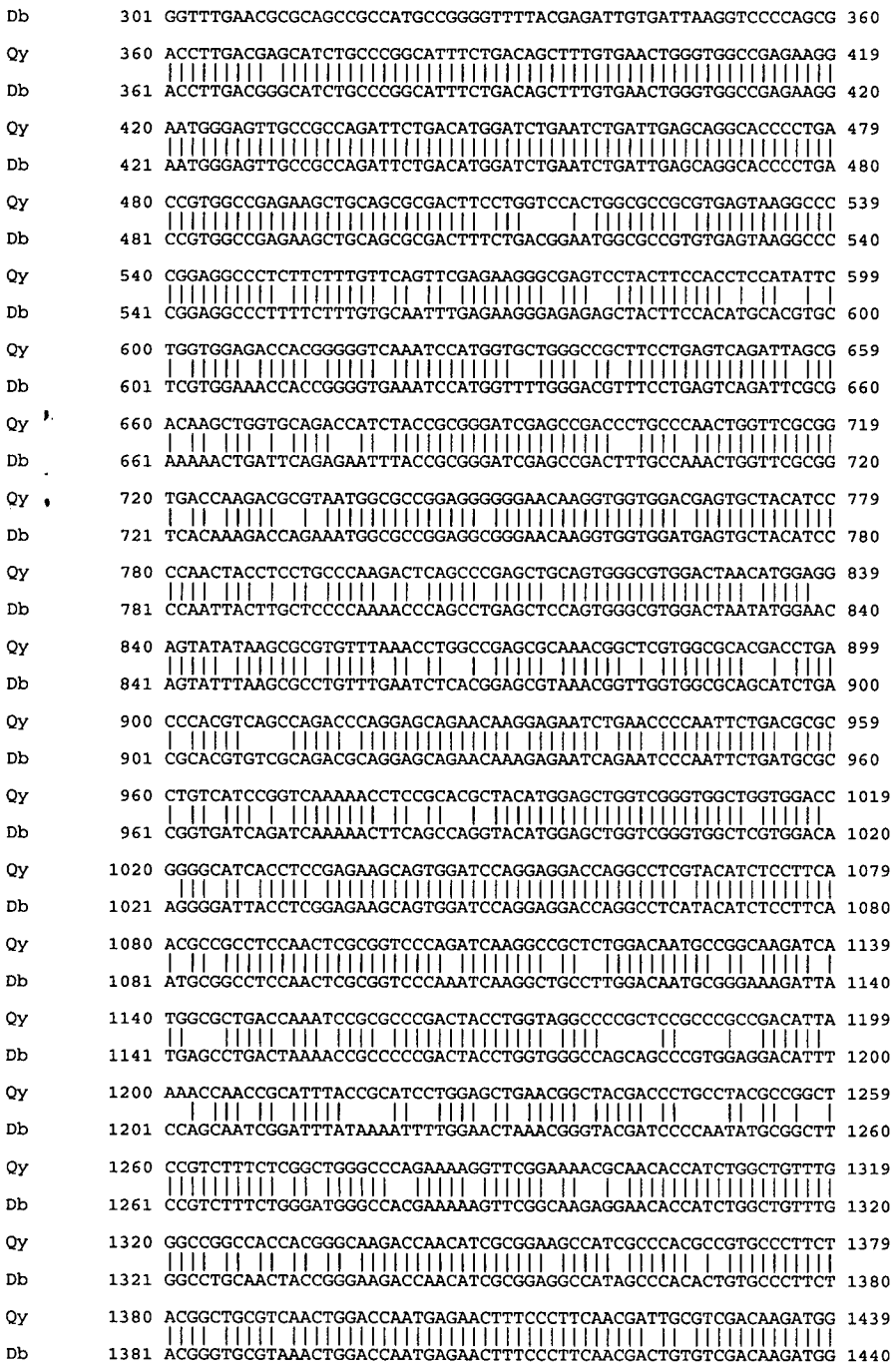
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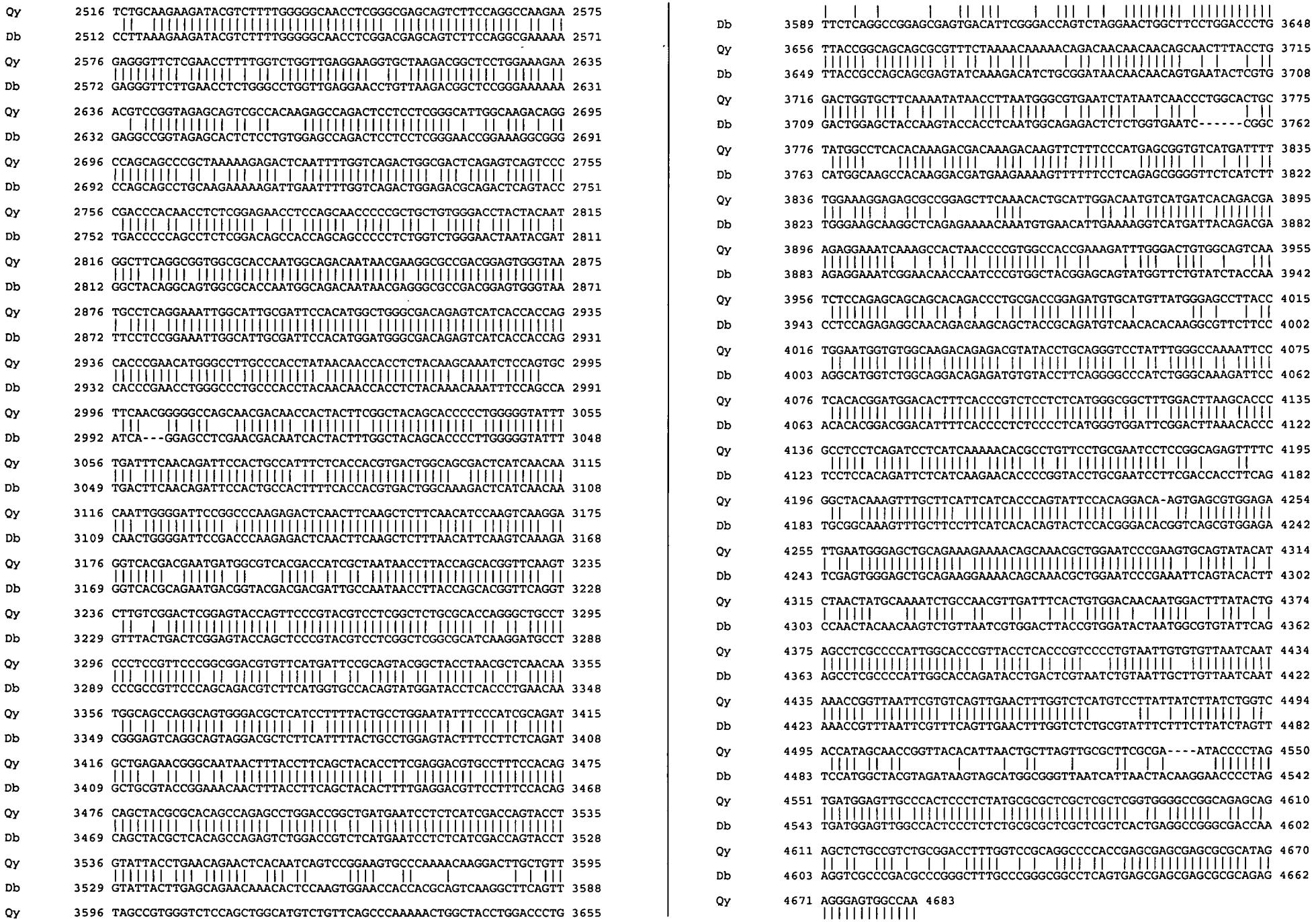
Db 2152 ATGTGGATTTGGATGACTGCATCTTTGAACAATAAATGATTTAAATCAGGTATGGCTGCC 2211
Qy 2217 GATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGGCAGTGGTGG 2276
Db 2212 GATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATAAGACAGTGGTGG 2271
Qy 2277 GACTTGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGG 2336
Db 2272 AAGCTCAAACCTGGCCCACCACCACCAAAGCCCGCAGAGCGGCATAAGGACGACAGCAGG 2331
Qy 2337 GGTCTGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAG 2396
Db 2332 GGTCTTGTGCTTCCTGGGTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGAGAG 2391
Qy 2397 CCCGTCAACGCGGCGGATGCAGCGGCCCTCGAGCACG-ACAAGGCCTACGACCAGCAGCT 2455
Db 2392 CCGGTCAACGAGGCAGACGCCGCGGCCCTCGAGCACGTACAAAGCCTACGACCGGCAGCT 2451
Qy 2456 CAAAGCGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCG 2515
Db 2452 CGACAGCGGAGACAACCCGTACCTCAAGTACAACCACGCCGACGCGGAGTTTCAGGAGCG 2511


Qy 2516 TCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAA 2575
Db 2512 CCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGCAGTCTTCCAGGCGAAAAA 2571
Qy 2576 GAGGGTTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCCTGGAAAGAA 2635
Db 2572 GAGGGTTCTTGAACCTCTGGGCCTGGTTGAGGAACCTGTTAAGACGGCTCCGGGAAAAAA 2631
Qy 2636 ACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGG 2695
Db 2632 GAGGCCGGTAGAGCACTCTCCTGTGGAGCCAGACTCCTCCTCGGGAACCGGAAAGGCGGG 2691
Qy 2696 CCAGCAGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCC 2755
Db 2692 CCAGCAGCCTGCAAGAAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACC 2751
Qy 2756 CGACCCACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAAT 2815
Db 2752 TGACCCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACTAATACGAT 2811
Qy 2816 GGCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAA 2875
Db 2812 GGCTACAGGCAGTGGCGCACCAATGGCAGACAATAACGAGGGCGCCGACGGAGTGGGTAA 2871
Qy 2876 TGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAG 2935
Db 2872 TTCCTCCGGAAATTGGCATTGCGATTCCACATGGATGGGCGACAGAGTCATCACCACCAG 2931
Qy 2936 CACCCGAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGC 2995
Db 2932 CACCCGAACCTGGGCCCTGCCCACCTACAACAACCACCTCTACAAACAAATTTCCAGCCA 2991
Qy 2996 TTCAACGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTT 3055
Db 2992 ATCA---GGAGCCTCGAACGACAATCACTACTTTGGCTACAGCACCCCTTGGGGGTATTT 3048
Qy 3056 TGATTTCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAA 3115
Db 3049 TGACTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAAAGACTCATCAACAA 3108
Qy 3116 CAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGA 3175
Db 3109 CAACTGGGGATTCCGACCCAAGAGACTCAACTTCAAGCTCTTTAACATTCAAGTCAAAGA 3168
Qy 3176 GGTCACGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGT 3235
Db 3169 GGTCACGCAGAATGACGGTACGACGACGATTGCCAATAACCTTACCAGCACGGTTCAGGT 3228
Qy 3236 CTTGTCGGACTCGGAGTACCAGTTCCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCT 3295
Db 3229 GTTTACTGACTCGGAGTACCAGCTCCCGTACGTCCTCGGCTCGGCGCATCAAGGATGCCT 3288
Qy 3296 CCCTCCGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAA 3355
Db 3289 CCCGCCGTTCCCAGCAGACGTCTTCATGGTGCCACAGTATGGATACCTCACCCTGAACAA 3348
Qy 3356 TGGCAGCCAGGCAGTGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGAT 3415
Db 3349 CGGGAGTCAGGCAGTAGGACGCTCTTCATTTTACTGCCTGGAGTACTTTCCTTCTCAGAT 3408
Qy 3416 GCTGAGAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAG 3475
Db 3409 GCTGCGTACCGGAAACAACTTTACCTTCAGCTACACTTTTGAGGACGTTCCTTTCCACAG 3468
Qy 3476 CAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCT 3535
Db 3469 CAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATCCTCTCATCGACCAGTACCT 3528
Qy 3536 GTATTACCTGAACAGAACTCACAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTT 3595
Db 3529 GTATTACTTGAGCAGAACAAACACTCCAAGTGGAACCACCACGCAGTCAAGGCTTCAGTT 3588
Qy 3596 TAGCCGTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTG 3655
Db 3589 TTCTCAGGCCGGAGCGAGTGACATTCGGGACCAGTCTAGGAACTGGCTTCCTGGACCCTG 3648
Qy 3656 TTACCGGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTG 3715
Db 3649 TTACCGCCAGCAGCGAGTATCAAAGACATCTGCGGATAACAACAACAGTGAATACTCGTG 3708
Qy 3716 GACTGGTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGC 3775
Db 3709 GACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATC------CGGC 3762
Qy 3776 TATGGCCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTT 3835
Db 3763 CATGGCAAGCCACAAGGACGATGAAGAAAAGTTTTTTCCTCAGAGCGGGGTTCTCATCTT 3822
Qy 3836 TGGAAAGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGA 3895
Db 3823 TGGGAAGCAAGGCTCAGAGAAAACAAATGTGAACATTGAAAAGGTCATGATTACAGACGA 3882
Qy 3896 AGAGGAAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAA 3955
Db 3883 AGAGGAAATCGGAACAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAA 3942
Qy 3956 TCTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACC 4015
Db 3943 CCTCCAGAGAGGCAACAGACAAGCAGCTACCGCAGATGTCAACACACAAGGCGTTCTTCC 4002
Qy 4016 TGGAATGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCC 4075
Db 4003 AGGCATGGTCTGGCAGGACAGAGATGTGTACCTTCAGGGGCCCATCTGGGCAAAGATTCC 4062
Qy 4076 TCACACGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCC 4135
Db 4063 ACACACGGACGGACATTTTCACCCCTCTCCCCTCATGGGTGGATTCGGACTTAAACACCC 4122
Qy 4136 GCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTC 4195
Db 4123 TCCTCCACAGATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCACCTTCAG 4182
Qy 4196 GGCTACAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACA-AGTGAGCGTGGAGA 4254
Db 4183 TGCGGCAAAGTTTGCTTCCTTCATCACACAGTACTCCACGGGACACGGTCAGCGTGGAGA 4242
Qy 4255 TTGAATGGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACAT 4314
Db 4243 TCGAGTGGGAGCTGCAGAAGGAAAACAGCAAACGCTGGAATCCCGAAATTCAGTACACTT 4302
Qy 4315 CTAACTATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTG 4374
Db 4303 CCAACTACAACAAGTCTGTTAATCGTGGACTTACCGTGGATACTAATGGCGTGTATTCAG 4362
Qy 4375 AGCCTCGCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAAT 4434
Db 4363 AGCCTCGCCCCATTGGCACCAGATACCTGACTCGTAATCTGTAATTGCTTGTTAATCAAT 4422
Qy 4435 AAACCGGTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTC 4494
Db 4423 AAACCGTTTAATTCGTTTCAGTTGAACTTTGGTCTCTGCGTATTTCTTTCTTATCTAGTT 4482
Qy 4495 ACCATAGCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGA----ATACCCCTAG 4550
Db 4483 TCCATGGCTACGTAGATAAGTAGCATGGCGGGTTAATCATTAACTACAAGGAACCCCTAG 4542
Qy 4551 TGATGGAGTTGCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAG 4610
Db 4543 TGATGGAGTTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAA 4602
Qy 4611 AGCTCTGCCGTCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAG 4670
Db 4603 AGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAG 4662
Qy 4671 AGGGAGTGGCCAA 4683

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Db       4663 AGGGAGTGGCCAA 4675


RESULT 2
US-11-327-357-2
; Sequence 2, Application US/11327357
; Publication No. US20060105983A1
; GENERAL INFORMATION:
;  APPLICANT: BTG International Ltd
;  APPLICANT:  BEARD DR, PETER
;  APPLICANT:  RAJ DR, KENNETH
;  TITLE OF INVENTION: CYTOTOXIC AGENTS
;  FILE REFERENCE: 142184WO
;  CURRENT APPLICATION NUMBER: US/11/327,357
;  CURRENT FILING DATE:  2006-01-09
;  PRIOR APPLICATION NUMBER: 0009887.1
;  PRIOR FILING DATE: 2000-04-20
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 145
;   TYPE: DNA
;   ORGANISM: adeno-associated virus 2
;   FEATURE:
;   NAME/KEY: misc_structure
;   LOCATION: (1)..(145)
;   OTHER INFORMATION: ITR
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (72)
;   OTHER INFORMATION: Unpaired base
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (94)
;   OTHER INFORMATION: Unpaired base
US-11-327-357-2

  Query Match             2.7%;  Score 125;  DB 7;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-24;
  Matches  125;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 80

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 140

Qy        121 GCCAA 125
              |||||
Db        141 GCCAA 145


RESULT 3
US-11-327-357-1/c
; Sequence 1, Application US/11327357
; Publication No. US20060105983A1
; GENERAL INFORMATION:
;  APPLICANT: BTG International Ltd
;  APPLICANT:  BEARD DR, PETER
;  APPLICANT:  RAJ DR, KENNETH
;  TITLE OF INVENTION: CYTOTOXIC AGENTS
;  FILE REFERENCE: 142184WO
;  CURRENT APPLICATION NUMBER: US/11/327,357
;  CURRENT FILING DATE:  2006-01-09
;  PRIOR APPLICATION NUMBER: 0009887.1
;  PRIOR FILING DATE: 2000-04-20
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4675
;   TYPE: DNA
;   ORGANISM: adeno-associated virus 2
US-11-327-357-1

  Query Match             2.5%;  Score 118.2;  DB 7;  Length 4675;
  Best Local Similarity   87.8%;  Pred. No. 1e-21;
  Matches  129;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||  ||  |||||  ||
Db       4675 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCAAAGCCCGGG 4616

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
              || ||  ||  |||||  ||  ||||||||||||||||||||||||||||||||||||||
Db       4615 CGTCGGGCGACCTTTGGTCGCCCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 4556

Qy        121 GCCAACTCCATCACTAGGGGTTCCTGG 147
              |||||||||||||||||||||||||| |
Db       4555 GCCAACTCCATCACTAGGGGTTCCTTG 4529


RESULT 4
US-11-327-357-2/c
; Sequence 2, Application US/11327357
; Publication No. US20060105983A1
; GENERAL INFORMATION:
;  APPLICANT: BTG International Ltd
;  APPLICANT:  BEARD DR, PETER
;  APPLICANT:  RAJ DR, KENNETH
;  TITLE OF INVENTION: CYTOTOXIC AGENTS
;  FILE REFERENCE: 142184WO
;  CURRENT APPLICATION NUMBER: US/11/327,357
;  CURRENT FILING DATE:  2006-01-09
;  PRIOR APPLICATION NUMBER: 0009887.1
;  PRIOR FILING DATE: 2000-04-20
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 145
;   TYPE: DNA
;   ORGANISM: adeno-associated virus 2
;   FEATURE:
;   NAME/KEY: misc_structure
;   LOCATION: (1)..(145)
;   OTHER INFORMATION: ITR
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (72)
;   OTHER INFORMATION: Unpaired base
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (94)
;   OTHER INFORMATION: Unpaired base
US-11-327-357-2

  Query Match             2.5%;  Score 117.8;  DB 7;  Length 145;
  Best Local Similarity   88.3%;  Pred. No. 2.2e-22;
  Matches  128;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||  ||  |||||  ||
Db        145 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCAAAGCCCGGG 86

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
              || ||  ||  |||||  ||  ||||||||||||||||||||||||||||||||||||||
Db         85 CGTCGGGCGACCTTTGGTCGCCCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 26

Qy        121 GCCAACTCCATCACTAGGGGTTCCT 145
              |||||||||||||||||||||||||
Db         25 GCCAACTCCATCACTAGGGGTTCCT 1


RESULT 5
US-11-269-117-6
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; Sequence 6, Application US/11269117
; Publication No. US20060110364A1
; GENERAL INFORMATION:
;  APPLICANT: LIN, et al.
;  TITLE OF INVENTION: VECTOR-MEDIATED DELIVERY OF POLYNUCLEOTIDES ENCODING SOLUBLE VEGF
;  TITLE OF INVENTION:  RECEPTORS
;  FILE REFERENCE: 28967/40835B
;  CURRENT APPLICATION NUMBER: US/11/269,117
;  CURRENT FILING DATE:  2005-11-08
;  PRIOR APPLICATION NUMBER: US 11/208,696
;  PRIOR FILING DATE: 2005-08-22
;  PRIOR APPLICATION NUMBER: US 60/602,926
;  PRIOR FILING DATE: 2004-08-20
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
;   LENGTH: 8322
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: AAV vector
US-11-269-117-6

  Query Match             2.3%;  Score 110;  DB 7;  Length 8322;
  Best Local Similarity   100.0%;  Pred. No. 2e-19;
  Matches  110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4625 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 4684

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAG 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4685 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAG 4734


RESULT 6
US-11-269-117-6/c
; Sequence 6, Application US/11269117
; Publication No. US20060110364A1
; GENERAL INFORMATION:
;  APPLICANT: LIN, et al.
;  TITLE OF INVENTION: VECTOR-MEDIATED DELIVERY OF POLYNUCLEOTIDES ENCODING SOLUBLE VEGF
;  TITLE OF INVENTION:  RECEPTORS
;  FILE REFERENCE: 28967/40835B
;  CURRENT APPLICATION NUMBER: US/11/269,117
;  CURRENT FILING DATE:  2005-11-08
;  PRIOR APPLICATION NUMBER: US 11/208,696
;  PRIOR FILING DATE: 2005-08-22
;  PRIOR APPLICATION NUMBER: US 60/602,926
;  PRIOR FILING DATE: 2004-08-20
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
;   LENGTH: 8322
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: AAV vector
US-11-269-117-6

  Query Match             2.3%;  Score 110;  DB 7;  Length 8322;
  Best Local Similarity   100.0%;  Pred. No. 2e-19;
  Matches  110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 57

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAG 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         56 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAG 7


RESULT 7
US-10-953-349-16574
; Sequence 16574, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16574
;   LENGTH: 1309
;   TYPE: DNA
;   ORGANISM: Glycine max
US-10-953-349-16574

  Query Match             1.1%;  Score 52;  DB 6;  Length 1309;
  Best Local Similarity   46.1%;  Pred. No. 0.00022;
  Matches  175;  Conservative    0;  Mismatches  205;  Indels    0;  Gaps    0;

Qy       1011 TGGTGGACCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACA 1070
              ||| ||| | || ||||   ||||    ||| |  |||   |  | |||   ||| | |
Db        638 TGGAGGAGCTGGTCATCCTGTCCGGCGCGCACTCCATCGGCGTCGGCCACTGCTCCTCCT 697

Qy       1071 TCTCCTTCAACGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCG 1130
              || ||  |  |  | || |   ||  |    | |  ||||  |  ||  |  |
Db        698 TCACCGGCCGCCTCACCGCGCCGCCGGAGCAGATCAACCCGGCCTACCGCAACCTTCTCA 757

Qy       1131 GCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCG 1190
              | | |       | |  |     | || ||| |  |     | ||| || |  |  |
Db        758 ACCACAAGTGCCACCAGGGCGCCAACCCGGCCGTCGTCAACAACGTCCGCGATGAGGACT 817

Qy       1191 CCGACATTAAAACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCT 1250
              ||| |       ||||  |||  | |  ||       | |    || |   |  | ||
Db        818 ACGAGACGGTGTCCAAGTTCATGCCCGGGTTCACCAGCCGGGTGCGCAAGATCAGCGACT 877

Qy       1251 ACGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCT 1310
              |  || |  |  |||   |  |      ||      ||| |||  |    |||| ||  ||
Db        878 TCCTCGACAACACCTTCTACCACAACAACCTCGCCAGGATCGTCAGCTTCAACTCCGACT 937

Qy       1311 GGCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCG 1370
              ||| | |   | |   |||| || || |  | || ||   ||   |  || | |||||
Db        938 GGCAGCTCATGACCCACACCGAGGCCAGGGGCCACGTCCACGAGTACGCCGACAACGCCA 997

Qy       1371 TGCCCTTCTACGGCTGCGTC 1390
              || ||   |||||  | ||
Db        998 CGCTCTGGGACGGCGACTTC 1017


RESULT 8
US-10-953-349-33293
; Sequence 33293, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33293
;   LENGTH: 1191
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-33293

  Query Match             1.0%;  Score 47.2;  DB 6;  Length 1191;
```

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  Best Local Similarity   44.3%;  Pred. No. 0.0039;
  Matches  193;  Conservative    0;  Mismatches  243;  Indels    0;  Gaps    0;

Qy       1009 GCTGGTGGACCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTA 1068
Db        473 GCTGGCGGGGAACAACCTGACGTACAAGGTCCCCGCGGGGCGGCGCGACGGGCGGGTGTC 532

Qy       1069 CATCTCCTTCAACGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGC 1128
Db        533 CAGGGACACGGACGCCAACAGCAACCTCCCCTCGCCGCTCTCCACCGCCGCCGAGCTCGT 592

Qy       1129 CGGCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCC 1188
Db        593 CGGCAACTTCACGCGCAAGAACCTCACCGCCGAGGACATGGTGGTGCTCTCCGGCGCGCA 652

Qy       1189 CGCCGACATTAAAACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGC 1248
Db        653 CACCGTCGGCCGCTCCCACTGCTCCTCCTTCACCAACCGCCTCTACGGCTTCAGCAACGC 712

Qy       1249 CTACGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCAT 1308
Db        713 CAGCGACGTCGACCCCACCATCAGCTCCGCCTACGCCCTCCTGCTGCGGGCCATCTGCCC 772

Qy       1309 CTGGCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGC 1368
Db        773 GTCCAACACCAGCCAGTTCTTCCCCAACACCACCACCGACATGGACCTCATCACGCCCGC 832

Qy       1369 CGTGCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGT 1428
Db        833 GCTGCTCGACAACAGGTACTACGTCGGCCTCGCCAACAACCTCGGCCTCTTCACGTCCGA 892

Qy       1429 CGACAAGATGGTGATC 1444
Db        893 CCAGGCTCTGCTCACC 908


RESULT 9
US-10-953-349-33793
; Sequence 33793, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33793
;   LENGTH: 1302
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-33793

  Query Match             1.0%;  Score 47;  DB 6;  Length 1302;
  Best Local Similarity   45.6%;  Pred. No. 0.0046;
  Matches  204;  Conservative    0;  Mismatches  240;  Indels    3;  Gaps    1;

Qy       1072 CTCCTTCAACGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGG 1131
Db        489 CGCCGCCGACGTCAACTCCCGCGCCGGCCCCACGGGGAAGACCGCGCTGCACCTGGCCGC 548

Qy       1132 CAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGC 1191
Db        549 CGAGATGGTCTCCC---CCGATATGGTGTCCGTGCTGCTTGACCACCACGCCGACCCCAG 605

Qy       1192 CGACATTAAAACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTA 1251
Db        606 CGCCAGGACGCTCGACGGCGTCACCCCGCTCGACGTGCTCCGAGGCCTCACATCAGAGTT 665

Qy       1252 CGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTG 1311
Db        666 CCTGTTCAAGGGCGCCGTGCCGGGGCTCACGCACATCGAGCCCAACAAGCTCAGGCTCTG 725

Qy       1312 GCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGT 1371
Db        726 CCTTGAGCTCGTGCAGTCCGCGGTGATGGTGACCACGCGCGACGTCGACGCCGCCGGCGA 785

Qy       1372 GCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGA 1431
Db        786 CGACGCCGGGGGAAGCGACGGCGGCGGCGGCGGCAACTTCCCCAGGAGCGACGCCGACGA 845

Qy       1432 CAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAA 1491
Db        846 CAGCTTGGTGAGCCTGACGATGAACTCCACGCTCATGTACCAGGGCCAGGAGATGGCGGC 905

Qy       1492 GGCCATTCTCGGCGGCAGCAAGGTGCG 1518
Db        906 TGCCGCGGTGGCCGCCGGTGAGGCGAG 932


RESULT 10
US-10-953-349-27324
; Sequence 27324, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27324
;   LENGTH: 845
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-27324

  Query Match             1.0%;  Score 46.6;  DB 6;  Length 845;
  Best Local Similarity   46.0%;  Pred. No. 0.0047;
  Matches  203;  Conservative    0;  Mismatches  229;  Indels    9;  Gaps    1;

Qy       1061 GCCTCGTACATCTCCTTCAACGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTG 1120
Db        249 GACTCCGAGCTCGCCCTCCACGCCGGGACGGACCGGCTCCGCCTCCTCGCCGGCGCGCCG 308

Qy       1121 GACAATGCCGGCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCC 1180
Db        309 GAGCTCTTCCCCGACCTGGTCCCGCTCGGCCTCGCCTCCTCCCTCTCCTCGCTCCTCACC 368

Qy       1181 GCTCCGCCCGCCGACATTAAAACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTAC 1240
Db        369 CACGAAAACGCCGACCTGGCCGCCGCGGCCGCTTCCCTCCTCGCCGACCTCACCGACTCC 428

Qy       1241 GACCCTGCCTACGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGC 1300
Db        429 GACGACCCCTCGGACCTCGCCGGGGTGCAGGCCCTCGCCGACGCGCTCGTCGACGCCAAC 488

Qy       1301 AACACCATCTGGCT---------GTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCG 1351
Db        489 GCGCTCGACCTGCTCGTGCACAACCTCTCGCGGCTCTCCGAGGTGGACCCCGACGAGGCC 548

Qy       1352 GAAGCCATCGCCCACGCCGTGCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTT 1411
Db        549 GAGGCGGTGCACCATTCCCTGGCCGTCCTCGAGAACCTCATCGACCTCCGCCCGCACCTC 608

Qy       1412 CCCTTCAACGATTGCGTCGACAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCC 1471
Db        609 GCCGACCTCGTCTGTGACCGCACCAAGGTGCTCCGGTGGCTGCTGGCCCGTGTCAAGGCC 668

Qy       1472 AAGGTCGTGGAGTCCGCCAAG 1492
Db        669 CGCGACTTCGAGGCCAACAAG 689
```

```
RESULT 11
US-10-513-348-6
; Sequence 6, Application US/10513348
; Publication No. US20060093589A1
; GENERAL INFORMATION:
;  APPLICANT: Warrington, Kenneth H.
;  APPLICANT:  Opie, Shaun R.
;  APPLICANT:  Muzyczka, Nicholas
;  TITLE OF INVENTION: VP2-MODIFIED RAAV VECTOR COMPOSITIONS AND USES THEREFOR
;  FILE REFERENCE: 4300.016100
;  CURRENT APPLICATION NUMBER: US/10/513,348
;  CURRENT FILING DATE:  2004-10-29
;  PRIOR APPLICATION NUMBER: PCT/US04/05205
;  PRIOR FILING DATE: 2004-02-19
;  PRIOR APPLICATION NUMBER: PCT/US03/13583
;  PRIOR FILING DATE: 2003-05-01
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 45
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-513-348-6

  Query Match             1.0%;  Score 45;  DB 6;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 0.0029;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2889 TGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACC 2933
             |||||||||||||||||||||||||||||||||||||||||||||
Db             1 TGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACC 45


RESULT 12
US-10-953-349-38921
; Sequence 38921, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38921
;   LENGTH: 2152
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
US-10-953-349-38921

  Query Match             0.9%;  Score 43.6;  DB 6;  Length 2152;
  Best Local Similarity   42.6%;  Pred. No. 0.048;
  Matches  284;  Conservative    0;  Mismatches  379;  Indels    3;  Gaps    1;

Qy        999 TGGTCGGGTGGCTGGTGGACCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACC 1058
              || ||  | |    |  |||  | ||| | |   | | ||    ||  | ||||| | |
Db        412 TGATCCCGGGCTCCGGCGACAAGCCCATGATCGGGGTGCAGTTCAGGGGCGAGGAGAAAC 471

Qy       1059 AGGCCTCGTACATCTCCTTCAACGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTC 1118
              ||  |||| |       ||| | ||     |       |     ||   | |||||
Db        472 AGTTCTCGGCCGAGGAGATCAGCTCCATGATCCTGAACAAGATGAAGGAGACGGCCGAGG 531

Qy       1119 TGGACAATGCCGGCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCC 1178
                ||   | |  ||  |||| |       |    |||  || | |||| |    | |
Db        532 CTTACCTCGGCACCACCATCAAGAACGCTGTCGTCACCGTCCCGGCCTACTTCAACGACT 591

Qy       1179 CCGCTCCGCCCGCCGACATTAAAACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCT 1238
              ||   |  |  |||  ||   |  ||  |  ||| | | || ||   | ` ||  |  |
Db        592 CCCAGCGCCAGGCCACCAAGGACGCCGGCGTCATCTCCGGCCTCAACGTCATGCGCATCA 651

Qy       1239 ACGACCCTGCCTACGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAAC 1298
              | ||    ||  |||||   || ||      |||     | | ||||   |  | | |
Db        652 TCAACGAGCCCACCGCCGCGGCCATCGCATACGGGCTCGACAAGAAGTCGAGCAGCGACG 711

Qy       1299 GCAACACCATCTGGCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCA 1358
              || | |  | |   ||  |          |  |   || |      || || ||     ||
Db        712 GCGAGAAGAACGTCCTCATCTTCGACCTCGGCGGCGGTACCTTTGACGTCTCGCTCCTCA 771

Qy       1359 TCGCCCACGCCGTGCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCA 1418
              |  | | |  |    |||  | | |   | || |     | |     || |       |
Db        772 CCATCGAGGAGGGCATCTTTGAGGTCAAGGCCACCGCCGGCGACACCCACCTGGGAGGCG 831

Qy       1419 ACGATTGCGTCGACAAGATGGTGATCTGGTGGG---AGGAGGGCAAGATGACGGCCAAGG 1475
              | || | || | ||  | | |||| |   |  |   |||||  ||||| || |  ||||
Db        832 AGGACTTCGACAACCGGCTCGTGAACCACTTCGTCCAGGAGTTCAAGAGGAAGAACAAGA 891

Qy       1476 TCGTGGAGTCCGCCAAGGCCATTCTCGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCA 1535
              |       | | |||  |||       | |  |   |  |  ||   | | | |   |
Db        892 AGGACATCACTGGCAACCCCAGGGCGCTCCGGCGACTGAGGACCGCCTGCGAGAGGGCTA 951

Qy       1536 AGTCGTCCGCCCAGATCGATCCCACCCCCGTGATCGTCACCTCCAACACCAACATGTGCG 1595
              ||  | |   |      |    ||    ||   |||| | | |     | |   | ||
Db        952 AGAGGACGCTCTCCTCCACCGCCCAAACCACCATCGAGATCGACTCGCTCTATGAGGGCA 1011

Qy       1596 CCGTGATTGACGGGAACAGCACCACCTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGT 1655
              ||    |  ||  || || ||||      |  |  | || |||       |||||   |
Db       1012 TCGACTTCTACACGACCATCACCCGTGCCCGGTTCGAGGAGCTCAACATGGACCTCTTCC 1071

Qy       1656 TCAAAT 1661
                 |||  |
Db       1072 GCAAGT 1077


RESULT 13
US-10-953-349-32310
; Sequence 32310, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32310
;   LENGTH: 1439
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-32310

  Query Match             0.9%;  Score 43.4;  DB 6;  Length 1439;
  Best Local Similarity   50.2%;  Pred. No. 0.044;
  Matches  107;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy       1312 GCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGT 1371
              |||| | |    | || |  ||| |  | | | || |       |   |||||  |   ||
Db        232 GCTGCTGGCCGTGTCCGCGGCGGACGCGGCGACCAGCAGCACGGTGGTCGCCGGCATGGT 291

Qy       1372 GCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGA 1431
              |  || | ||   |||     || |  ||     |     |||   || |       | ||  |
Db        292 GTTCTGCGACCAGTGCAAGGACGGCGCCCGCGGCCTCTTCGACTACCCGCTCTACGGGGC 351

Qy       1432 CAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAA 1491
                | ||| ||||  ||| |  |  ||| | |   ||  || |||   |||||  |  ||
Db        352 GCGGGTGGCGATCCAGTGCGGCGGCGGCGACACCCCGATCACGGTGCGGGAGTGCAACAC 411

Qy       1492 GGCCATTCTCGGCGGCAGCAAGGTGCGCGTGGA 1524
                 |    |||||||  |   |||||| ||||
```

```
Db        412 CAACTGGTTCGGCGGCTTCTCCGTGCGCATGGA 444


RESULT 14
US-10-513-348-1
; Sequence 1, Application US/10513348
; Publication No. US20060093589A1
; GENERAL INFORMATION:
;  APPLICANT: Warrington, Kenneth H.
;  APPLICANT:  Opie, Shaun R.
;  APPLICANT:  Muzyczka, Nicholas
;  TITLE OF INVENTION: VP2-MODIFIED RAAV VECTOR COMPOSITIONS AND USES THEREFOR
;  FILE REFERENCE: 4300.016100
;  CURRENT APPLICATION NUMBER: US/10/513,348
;  CURRENT FILING DATE:  2004-10-29
;  PRIOR APPLICATION NUMBER: PCT/US04/05205
;  PRIOR FILING DATE: 2004-02-19
;  PRIOR APPLICATION NUMBER: PCT/US03/13583
;  PRIOR FILING DATE: 2003-05-01
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 48
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-513-348-1

  Query Match             0.9%;  Score 43.2;  DB 6;  Length 48;
  Best Local Similarity   93.8%;  Pred. No. 0.0091;
  Matches   45;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2194 GACTTAAACCAGGTATGGCTGCCGATGGTTATCTTCCAGATTGGCTCG 2241
             || ||||| ||||| |||||||||||||||||||||||||||||||||
Db          1 GATTTAAATCAGGTCTGGCTGCCGATGGTTATCTTCCAGATTGGCTCG 48


RESULT 15
US-10-984-694-2
; Sequence 2, Application US/10984694
; Publication No. US20060099679A1
; GENERAL INFORMATION:
;  APPLICANT: TSIEN, Roger Y.
;  APPLICANT:  WANG, Lei
;  TITLE OF INVENTION: METHODS FOR ENGINEERING POLYPEPTIDE
;  TITLE OF INVENTION:  VARIANTS VIA SOMATIC HYPERMUTATION AND POLYPEPTIDES MADE
;  TITLE OF INVENTION:  THEREBY
;  FILE REFERENCE: 39754-0976A US
;  CURRENT APPLICATION NUMBER: US/10/984,694
;  CURRENT FILING DATE:  2004-11-08
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 681
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleic acid encoding the fluorescent protein
;   OTHER INFORMATION: mRFP1.2
US-10-984-694-2

  Query Match             0.9%;  Score 43.2;  DB 6;  Length 681;
  Best Local Similarity   44.5%;  Pred. No. 0.034;
  Matches  171;  Conservative    0;  Mismatches  213;  Indels    0;  Gaps    0;

Qy       1018 CCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTT 1077
              || |  | || |||  || |  | ||     |||       | | |||  |   || | |
Db        162 CCTGCCCTTCGCCTGGGACATCCTGTCCCCTCAGTTCATGTACGGCTCCAAGGCCTACGT 221

Qy       1078 CAACGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGAT 1137
               ||   | || || ||   |    | |  | |||    |  |   | | | |  ||||
Db        222 GAAGCACCCCGCCGACATCCCCGACTACTTGAAGCTGTCCTTCCCCGAGGGCTTCAAGTG 281

Qy       1138 CATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACAT 1197
                |   ||| || | || |  || |  | ||||   |    | | |  | ||  | |
Db        282 GGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGGTGACCGTGACCCAGGACTCCTCCCT 341

Qy       1198 TAAAACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGG 1257
                |   |  |    |  |  ||   || |||||  ||||  | ||    ||| || |||
Db        342 GCAGGACGGCGAGTTCATCTACAAGGTGAAGCTGCGCGGCACCAACTTCCCCTCCGACGG 401

Qy       1258 CTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTT 1317
              | ||||  | |        | ||  |    ||   |        | |    || | |
Db        402 CCCCGTAATGCAGAAGAAGACCATGGGCTGGGAGGCCTCCTCCGAGCGGATGTACCCCGA 461

Qy       1318 TGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTT 1377
                |     |||   | |||| ||| ||| ||   |        |     ||| ||  | ||
Db        462 GGACGGCGCCCTGAAGGGCGAGATCAAGATGAGGCTGAAGCTGAAGGACGGCGGCCACTA 521

Qy       1378 CTACGGCTGCGTCAACTGGACCAA 1401
              | ||| |   |||||    ||| |
Db        522 CGACGCCGAGGTCAAGACCACCTA 545


Search completed: June 13, 2006, 13:22:07
Job time : 152 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 12:06:09 ; Search time 2682 Seconds
(without alignments)
12174.139 Million cell updates/sec

Title: US-10-696-261-19
Perfect score: 4683
Sequence: 1 ttggccactccctctctgcg.....cgcatagagggagtggccaa 4683

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
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8: geneseqn2003as:*
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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4663.8	99.6	4683	4	AAF23749	Aaf23749 AAV6 DNA
2	4663.8	99.6	4683	10	ADL13983	Adl13983 Adeno-ass
3	4663.8	99.6	4683	12	ADG39763	Adg39763 AAV-6 gen
4	4253.2	90.8	4718	3	AAD00772	Aad00772 Adeno-ass
5	4253.2	90.8	4718	10	ADE76507	Ade76507 Adeno-ass
6	4253.2	90.8	4718	10	ADL13984	Adl13984 Adeno-ass
7	4253.2	90.8	4718	12	ADG39758	Adg39758 AAV-1 gen
8	3831.4	81.8	4239	13	ADW39402	Adw39402 Adeno-ass
9	3831.4	81.8	4239	14	ADZ46598	Adz46598 HSV-AAV s
10	3802	81.2	4347	13	ADW39398	Adw39398 Adeno-ass
11	3802	81.2	4347	14	ADZ46594	Adz46594 HSV-AAV s
12	3802	81.2	4347	14	AEF81093	Aef81093 Adeno-ass
13	3678.4	78.5	4721	10	ADE76502	Ade76502 Adeno-ass
14	3678.4	78.5	4721	12	ADG39764	Adg39764 AAV-7 gen
15	3678.4	78.5	4721	14	ADV67509	Adv67509 Nucleotid
16	3678.4	78.5	4721	14	ADZ27030	Adz27030 Adeno-ass
17	3443.2	73.5	4382	9	ABQ80410	Abq80410 AAV9 rep
18	3404.6	72.7	4385	10	ADE76506	Ade76506 Adeno-ass
19	3370.4	72.0	4393	9	ACF05811	Acf05811 Adeno ass
20	3370.4	72.0	4393	10	ADE76505	Ade76505 Adeno-ass
21	3370.4	72.0	4393	12	ADG39765	Adg39765 AAV-8 gen
22	3370.4	72.0	4393	14	ADV67510	Adv67510 Nucleotid
23	3370.4	72.0	4393	14	ADZ27032	Adz27032 Adeno-ass
24	3296.2	70.4	4679	4	AAI66974	Aai66974 Adeno-ass
25	3296.2	70.4	4679	6	ABK89694	Abk89694 Adeno-ass
26	3296.2	70.4	4679	10	ABV76133	Abv76133 Adeno ass
27	3296.2	70.4	4679	14	AEA48850	Aea48850 Bovine ad
28	3296.2	70.4	8698	4	AAH26325	Aah26325 Wild-type
29	3294.6	70.4	4679	4	AAF23750	Aaf23750 AAV2 DNA
30	3285	70.1	4679	12	ADG39757	Adg39757 AAV-2 gen
31	3270.8	69.8	4680	2	AAT09008	Aat09008 Wild-type
32	3270.8	69.8	4680	8	ABX14497	Abx14497 Wild-type
33	3270.8	69.8	4680	9	ADA50070	Ada50070 Adeno-ass
34	3270.8	69.8	4680	10	ADE81075	Ade81075 Adeno-ass
35	3270.8	69.8	4680	12	ADG92079	Adg92079 Wild-type
36	3270.8	69.8	4680	14	AEB48083	Aeb48083 Adeno-ass
37	3244.2	69.3	4675	4	AAH41481	Aah41481 Adeno-ass
38	3244.2	69.3	4675	4	AAF89931	Aaf89931 Nucleotid
39	3244.2	69.3	4675	6	ABA02989	Aba02989 Adeno-ass
40	3244.2	69.3	4675	6	ABS69879	Abs69879 Human ade
41	3244.2	69.3	4675	6	ABS69880	Abs69880 Human ade
42	3244.2	69.3	4675	10	ADE76508	Ade76508 Adeno-ass
43	3244.2	69.3	4675	15	AEF10041	Aef10041 Adeno-ass
44	3244.2	69.3	4675	15	AEF10040	Aef10040 Adeno-ass
45	3182.8	68.0	4722	4	AAF23748	Aaf23748 AAV3B DNA

ALIGNMENTS

RESULT 1
AAF23749
ID AAF23749 standard; DNA; 4683 BP.
XX
AC AAF23749;
XX
DT 28-MAR-2001 (first entry)
XX
DE AAV6 DNA sequence.
XX
KW AAV6; gene therapy; AAV viral vector; cystic fibrosis; cancer; AIDS;
KW atherosclerosis; sickle cell anaemia; thalassaemia;
KW blood clotting disorder; diabetes; ss.
XX
OS Adeno associated virus.
XX
PN US6156303-A.
XX
PD 05-DEC-2000.
XX
PF 11-JUN-1997; 97US-00873168.
XX
PR 11-JUN-1997; 97US-00873168.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Russell DW, Rutledge EA;
XX
DR WPI; 2001-060164/07.
XX
PT Adeno-associated virus serotype 6 and viral vector derived from it for
PT gene therapy of cystic fibrosis, cancer, acquired immunodeficiency
PT syndrome, sickle cell anemia, thalassemia and diabetes.
XX
PS Claim 1; Fig 1; 50pp; English.
XX
CC The present invention relates to adeno-associated virus serotypes. The
CC present sequence is the DNA sequence of one such serotype (AAV6). AAV6
CC can be used to contruct AAV viral vectors for use in gene therapy for a
CC range of disorders: cystic fibrosis, cancer, AIDS, atherosclerosis,
CC sickle cell anaemia, thalassaemia, blood clotting disorders and diabetes.

CC The AAV viral vectors have increased transduction efficiency of a
CC particular host cell as the AAV virion containing the AAV vector genome
CC can be modified to express a capsid protein of an AAV serotype that
CC transduces the selected host cell
XX
SQ Sequence 4683 BP; 1114 A; 1363 C; 1277 G; 929 T; 0 U; 0 Other;

Query Match 99.6%; Score 4663.8; DB 4; Length 4683;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 4671; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Db          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
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Qy        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180

Qy        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        481 CGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCGCCGCGTGAGTAAGGCCCC 540
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Db        901 CCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGCC 960

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Qy       1081 CGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCAT 1140

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Qy       1201 AACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCTC 1260
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Qy       1741 GGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAACAG 1800
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Qy       1801 ACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1861 TCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGCCGACAGGTACCAAAACAA 1920
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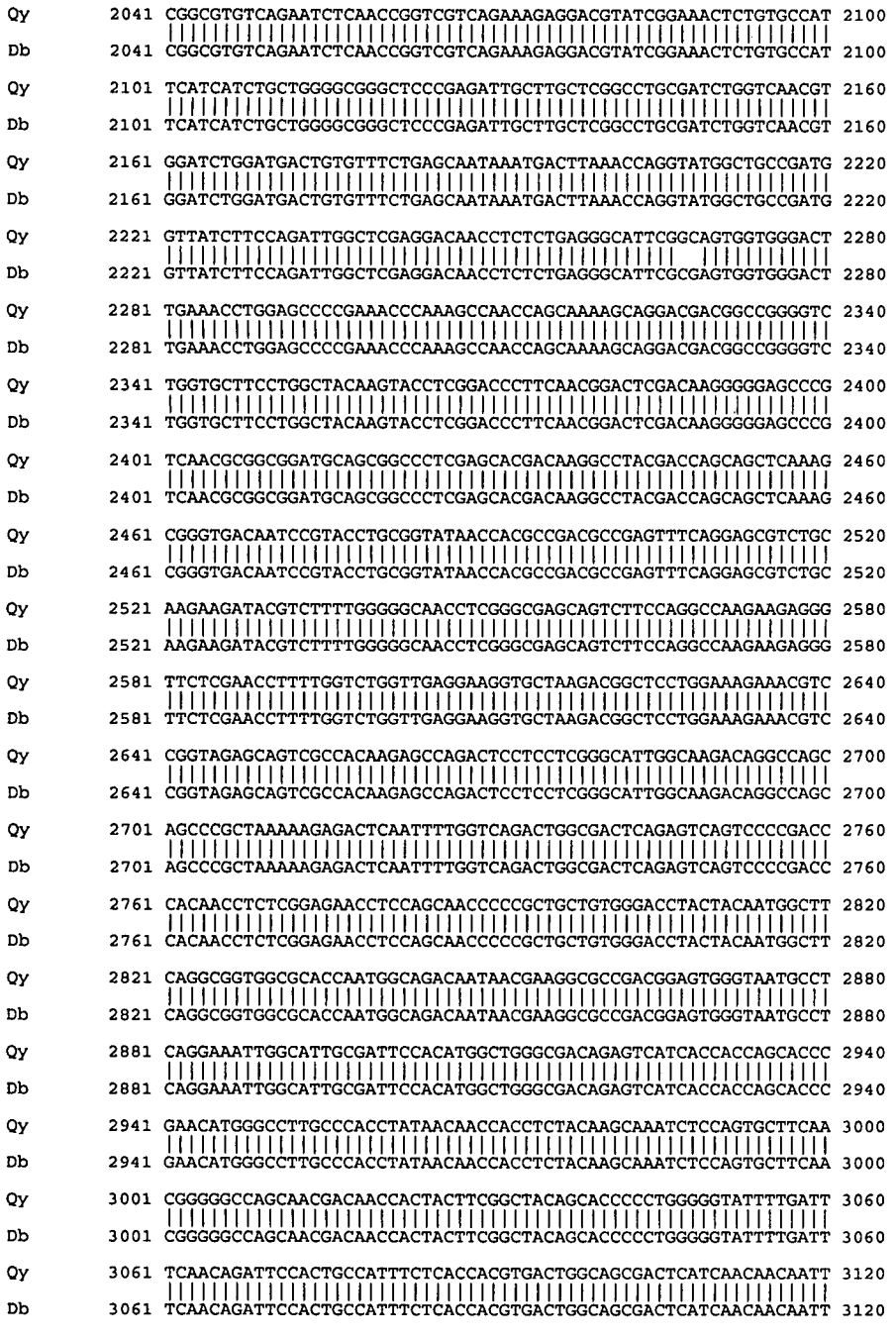
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Db 2101 TCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGT 2160
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Qy 2401 TCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAG 2460
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Qy 3001 CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATT 3060
Db 3001 CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATT 3060
Qy 3061 TCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATT 3120
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Qy 3361 GCCAGGCAGTGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGA 3420
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Db 3421 GAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCT 3480
Qy 3481 ACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATT 3540
Db 3481 ACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATT 3540
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Qy 3661 GGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTG 3720
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Db 3901 AAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCC 3960
Qy 3961 AGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAA 4020
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Qy       4321 ATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTC 4380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 ATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTC 4380

Qy       4381 GCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCG 4440
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                ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
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Qy       4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCG 4620
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 TCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGG 4680

Qy       4681 CAA 4683
                |||
Db       4681 CAA 4683
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RESULT 2
ADL13983
ID ADL13983 standard; DNA; 4683 BP.
XX
AC ADL13983;
XX
DT 06-MAY-2004 (first entry)
XX
DE Adeno-associated virus serotype 6 complete DNA.
XX
KW ss; cytostatic; neuroprotective; antiinflammatory; gene therapy;
KW expression construct; adeno-associated virus;
KW integration efficiency element; inverted terminal repeat; integration;
KW chromosome; cancer; lymphoma; leukemia; multiple myeloma; neuroblastoma;
KW retinoblastoma; inflammatory disease; arthritis;
KW neurodegenerative disease.
XX
OS Adeno-associated virus 6.
XX
PN WO2003087334-A2.
XX
PD 23-OCT-2003.
XX
PF 09-APR-2003; 2003WO-US011191.
XX
PR 09-APR-2002; 2002US-0371044P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Falck-Pedersen ES, Philpott N;
XX
DR WPI; 2003-833723/77.
XX
PT New expression construct comprising a nucleic acid sequence encoding an
PT adeno-associated virus integration efficiency element, useful for
PT treating cancer e.g. lung cancer or colon cancer or inflammatory disease
PT e.g. arthritis.
XX
PS Disclosure; SEQ ID NO 2; 62pp; English.
XX
CC The invention relates to an expression construct comprising a nucleic
CC acid sequence encoding an adeno-associated virus integration efficiency
CC element (AAV IEE), which is devoid of AAV inverted terminal repeats (AAV
CC ITRs) and site-specifically integrates into a host cell chromosome when
CC provided to the host cell in conjunction with an AAV Rep protein. The
CC expression construct can be used as a therapeutic factor for treating a
CC mammal for a pathologic state which is cancer, including lung cancer,
CC colon cancer, renal cancer, anal cancer, bile duct cancer, bladder
CC cancer, bone cancer, brain cancer, spinal chord cancer, breast cancer,
CC cervical cancer, lymphoma, endometrial cancer, esophageal cancer,
CC gallbladder cancer, gastrointestinal cancer, laryngeal cancer, leukemia,
CC liver cancer, multiple myeloma, neuroblastoma, ovarian cancer, pancreatic
CC cancer, prostatic cancer, retinoblastoma, skin cancer, stomach cancer,
CC testicular cancer, thymus cancer or thyroid cancer. Other pathologic
CC state includes inflammatory disease (arthritis), neurodegenerative
CC disease, a disease of an organ attributed to the presence of increased or
CC decreased level of a particular gene product(s). This sequence
CC corresponds to the AAV serotype 6 complete DNA including the IEE
CC sequence.
XX
SQ Sequence 4683 BP; 1114 A; 1363 C; 1277 G; 929 T; 0 U; 0 Other;

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  Query Match             99.6%;  Score 4663.8;  DB 10;  Length 4683;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 4671;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

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Db          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120

Qy        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180

Qy        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240

Qy        241 GTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGA 300

Qy        301 GGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGA 360

Qy        361 CCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGA 420

Qy        421 ATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGAC 480

Qy        481 CGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCGCCGCGTGAGTAAGGCCCC 540
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        481 CGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCAGTGGCGCCGCGTGAGTAAGGCCCC 540

Qy        541 GGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTACTTCCACCTCCATATTCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTACTTCCACCTCCATATTCT 600

Qy        601 GGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGCGA 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        601 GGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGGGA 660
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Qy       661 CAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCTGCCCAACTGGTTCGCGGT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCTGCCCAACTGGTTCGCGGT 720

Qy       721 GACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCCC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 GACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCCC 780

Qy       781 CAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGGA 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGGA 840

Qy       841 GTATATAAGCGCGTGTTTAAACCTGGCCGAGCGCAAACGGCTCGTGGCGCACGACCTGAC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 GTATATAAGCGCGTGTTTAAACCTGGCCGAGCGCAAACGGCTCGTGGCGCACGACCTGAC 900

Qy       901 CCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGCC 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 CCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGCC 960

Qy       961 TGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACCG 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 TGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACCG 1020

Qy      1021 GGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCAA 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCAA 1080

Qy      1081 CGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCAT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCAT 1140

Qy      1141 GGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACATTAA 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 GGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACATTAA 1200

Qy      1201 AACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCTC 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 AACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCTC 1260

Qy      1261 CGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTTTGG 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 CGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTTTGG 1320

Qy      1321 GCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCTA 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 GCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCTA 1380

Qy      1381 CGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGGT 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 CGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGGT 1440

Qy      1441 GATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTCT 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 GATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTCT 1500

Qy      1501 CGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTCCGCCCAGATCGATCCCAC 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 CGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTCCGCCCAGATCGATCCCAC 1560

Qy      1561 CCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACAGCACCAC 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 CCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACAGCACCAC 1620

Qy      1621 CTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATTTGAACTCACCCGCCGTCT 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 CTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATTTGAACTCACCCGCCGTCT 1680

Qy      1681 GGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGAGTTCTTCCGCTGGGCGCA 1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 GGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGAGTTCTTCCGCTGGGCGCA 1740

Qy      1741 GGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAACAG 1800
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            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 GGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAAGAG 1800

Qy      1801 ACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGA 1860
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 ACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGA 1860

Qy      1861 TCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGCCGACAGGTACCAAAACAA 1920
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 TCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGCCGACAGGTACCAAAACAA 1920

Qy      1921 ATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGAAT 1980
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 ATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGAAT 1980

Qy      1981 GAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGACTGTTCAGAATGTTTCCC 2040
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 GAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGACTGTTCAGAATGTTTCCC 2040

Qy      2041 CGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCAT 2100
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 CGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCAT 2100

Qy      2101 TCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGT 2160
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 TCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGT 2160

Qy      2161 GGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAACCAGGTATGGCTGCCGATG 2220
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 GGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAACCAGGTATGGCTGCCGATG 2220

Qy      2221 GTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGGCAGTGGTGGGACT 2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 GTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGGACT 2280

Qy      2281 TGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTC 2340
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 TGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTC 2340

Qy      2341 TGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCG 2400
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 TGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCG 2400

Qy      2401 TCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAG 2460
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 TCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAG 2460

Qy      2461 CGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGC 2520
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 CGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGC 2520

Qy      2521 AAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGAGGG 2580
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 AAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGAGGG 2580

Qy      2581 TTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCCTGGAAAGAAACGTC 2640
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 TTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCCTGGAAAGAAACGTC 2640

Qy      2641 CGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGC 2700
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641 CGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGC 2700

Qy      2701 AGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACC 2760
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 AGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACC 2760

Qy      2761 CACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTT 2820
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761 CACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTT 2820

Qy      2821 CAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCT 2880
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2821 CAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCT 2880
Qy       2881 CAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCC 2940
Db       2881 CAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCC 2940
Qy       2941 GAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAA 3000
Db       2941 GAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAA 3000
Qy       3001 CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATT 3060
Db       3001 CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATT 3060
Qy       3061 TCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATT 3120
Db       3061 TCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATT 3120
Qy       3121 GGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCA 3180
Db       3121 GGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCA 3180
Qy       3181 CGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTGT 3240
Db       3181 CGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTCT 3240
Qy       3241 CGGACTCGGAGTACCAGTTCCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTC 3300
Db       3241 CGGACTCGGAGTACCAGTTGCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTC 3300
Qy       3301 CGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCA 3360
Db       3301 CGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCA 3360
Qy       3361 GCCAGGCAGTGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGA 3420
Db       3361 GCCAGGCAGTGGGACGGTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGA 3420
Qy       3421 GAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCT 3480
Db       3421 GAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCT 3480
Qy       3481 ACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATT 3540
Db       3481 ACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATT 3540
Qy       3541 ACCTGAACAGAACTCACAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCC 3600
Db       3541 ACCTGAACAGAACTCAGAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCC 3600
Qy       3601 GTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACC 3660
Db       3601 GGGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACC 3660
Qy       3661 GGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTG 3720
Db       3661 GGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTG 3720
Qy       3721 GTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGG 3780
Db       3721 GTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGG 3780
Qy       3781 CCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAA 3840
Db       3781 CCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAA 3840
Qy       3841 AGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGG 3900
Db       3841 AGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGG 3900
Qy       3901 AAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCC 3960
Db       3901 AAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCC 3960
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Qy       3961 AGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAA 4020
Db       3961 AGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAA 4020
Qy       4021 TGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACA 4080
Db       4021 TGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACA 4080
Qy       4081 CGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTC 4140
Db       4081 CGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTC 4140
Qy       4141 CTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTA 4200
Db       4141 CTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTA 4200
Qy       4201 CAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAAT 4260
Db       4201 CAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAAT 4260
Qy       4261 GGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACT 4320
Db       4261 GGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACT 4320
Qy       4321 ATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTC 4380
Db       4321 ATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTC 4380
Qy       4381 GCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCG 4440
Db       4381 GCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCG 4440
Qy       4441 GTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCACCATA 4500
Db       4441 GTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCGTTATTATCTTATCTGGTCACCATA 4500
Qy       4501 GCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGAATACCCCTAGTGATGGAGTT 4560
Db       4501 GCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGAATACCCCTAGTGATGGAGTT 4560
Qy       4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCG 4620
Db       4561 GCCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCG 4620
Qy       4621 TCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGC 4680
Db       4621 TCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGG 4680
Qy       4681 CAA 4683
Db       4681 CAA 4683
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RESULT 3
ADG39763
ID   ADG39763 standard; DNA; 4683 BP.
XX
AC   ADG39763;
XX
DT   11-MAR-2004  (first entry)
XX
DE   AAV-6 genomic DNA sequence SEQ ID NO:25.
XX
KW   parvovirus; rep; cap; DNA binding domain; capsid interacting domain;
KW   recombinant hybrid parvovirus particle;
KW   recombinant adeno-associated virus; rAAV; AAV; vaccine; gene therapy;
KW   gene; ds.
XX
OS   Adeno-associated virus 6.
XX
PN   WO2003104392-A2.
XX
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PD 18-DEC-2003.
XX
PF 02-DEC-2002; 2002WO-US038423.
XX
PR 18-DEC-2001; 2001US-0341919P.
XX
PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Samulski RJ, Rabinowitz JE;
XX
DR WPI; 2004-062324/06.
XX
PT New polynucleotides comprising parvovirus rep coding sequences and
PT parvovirus cap coding sequences, useful in producing higher stocks of
PT hybrid parvovirus vectors for delivering therapeutic nucleic acids to a
PT subject.
XX
PS Disclosure; SEQ ID NO 25; 115pp; English.
XX
CC The present invention describes a polynucleotide (I), comprising
CC parvovirus rep coding sequences and parvovirus cap coding sequences. The
CC rep coding sequences encodes a DNA binding domain from a first
CC parvovirus, and a capsid interacting domain from a parvovirus different
CC from the first parvovirus. The cap coding sequence comprises sequences
CC from the different parvovirus. Also described: (1) a vector comprising
CC (I); (2) a cell comprising (I), or parvovirus rep coding sequences and
CC parvovirus cap coding sequences, where the rep coding sequences encode a
CC DNA binding domain from a first parvovirus and a capsid interacting
CC domain from a parvovirus different from the first parvovirus, the cap
CC coding sequences comprise sequences from the different parvovirus, and
CC the rep coding sequences are stably integrated into the genome of the
CC cell; and (3) producing a recombinant hybrid parvovirus particle or adeno
CC -associated virus (rAAV) particle. (I) can be used in vaccines, and in
CC gene therapy. The polynucleotide (I) can be used in producing higher
CC stocks of hybrid parvoviruses or parvovirus vectors, which may be used in
CC the delivery of nucleic acids having biological effect to treat or
CC ameliorate the symptoms associated with any disorder related to gene
CC expression. The polynucleotide may be used to produce a parvovirus vector
CC to express an immunogenic polypeptide in a subject, e.g. for vaccination.
CC The parvovirus vector may also be used to provide an antisense nucleic
CC acid to a cell in vitro or in vivo, or in diagnostic and screening
CC methods. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 4683 BP; 1114 A; 1363 C; 1277 G; 929 T; 0 U; 0 Other;

Query Match 99.6%; Score 4663.8; DB 12; Length 4683;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 4671; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120

Qy        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCAACTCCATCACTAGGGGTTCCTGGAGGGGTGGAGTCGTGACGTGAATTACGTCATAG 180

Qy        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCAT 240

Qy        241 GTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 GGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 CCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGA 420

Qy        421 ATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGAC 480

Qy        481 CGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCGCCGCGTGAGTAAGGCCCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCAGTGGCGCCGCGTGAGTAAGGCCCC 540

Qy        541 GGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTACTTCCACCTCCATATTCT 600
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Qy        601 GGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGCGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        601 GGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGGGA 660

Qy        661 CAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCTGCCCAACTGGTTCGCGGT 720
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Qy        721 GACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCCC 780

Qy        781 CAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        841 GTATATAAGCGCGTGTTTAAACCTGGCCGAGCGCAAACGGCTCGTGGCGCACGACCTGAC 900
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Qy        901 CCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGCC 960
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Qy        961 TGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACCG 1020
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Qy       1021 GGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCAA 1080

Qy       1081 CGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCAT 1140
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Db       1081 CGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCAT 1140

Qy       1141 GGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACATTAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1201 AACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCTC 1260
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Qy       1321 GCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCTA 1380
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Db       1321 GCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCTA 1380

Qy       1381 CGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGGT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGGT 1440
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Qy       1441 GATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTCT 1500
Db       1441 GATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTCT 1500

Qy       1501 CGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTCCGCCCAGATCGATCCCAC 1560
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Qy       1561 CCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACAGCACCAC 1620
Db       1561 CCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACAGCACCAC 1620

Qy       1621 CTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATTTGAACTCACCCGCCGTCT 1680
Db       1621 CTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATTTGAACTCACCCGCCGTCT 1680

Qy       1681 GGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGAGTTCTTCCGCTGGGCGCA 1740
Db       1681 GGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGAGTTCTTCCGCTGGGCGCA 1740

Qy       1741 GGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAACAG 1800
Db       1741 GGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAAGAG 1800

Qy       1801 ACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGA 1860
Db       1801 ACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGA 1860

Qy       1861 TCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGCCGACAGGTACCAAAACAA 1920
Db       1861 TCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGCCGACAGGTACCAAAACAA 1920

Qy       1921 ATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGAAT 1980
Db       1921 ATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGAAT 1980

Qy       1981 GAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGACTGTTCAGAATGTTTCCC 2040
Db       1981 GAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGACTGTTCAGAATGTTTCCC 2040

Qy       2041 CGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCAT 2100
Db       2041 CGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCAT 2100

Qy       2101 TCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGT 2160
Db       2101 TCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGT 2160

Qy       2161 GGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAACCAGGTATGGCTGCCGATG 2220
Db       2161 GGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAACCAGGTATGGCTGCCGATG 2220

Qy       2221 GTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGGCAGTGGTGGGACT 2280
Db       2221 GTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGGACT 2280

Qy       2281 TGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTC 2340
Db       2281 TGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTC 2340

Qy       2341 TGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCG 2400
Db       2341 TGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCG 2400

Qy       2401 TCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAG 2460
Db       2401 TCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAG 2460

Qy       2461 CGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGC 2520
Db       2461 CGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGC 2520

Qy       2521 AAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGAGGG 2580
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Db       2521 AAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGAGGG 2580

Qy       2581 TTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCCTGGAAAGAAACGTC 2640
Db       2581 TTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCCTGGAAAGAAACGTC 2640

Qy       2641 CGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGC 2700
Db       2641 CGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGC 2700

Qy       2701 AGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACC 2760
Db       2701 AGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACC 2760

Qy       2761 CACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTT 2820
Db       2761 CACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTT 2820

Qy       2821 CAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCT 2880
Db       2821 CAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCT 2880

Qy       2881 CAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCC 2940
Db       2881 CAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCC 2940

Qy       2941 GAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAA 3000
Db       2941 GAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAA 3000

Qy       3001 CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATT 3060
Db       3001 CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATT 3060

Qy       3061 TCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATT 3120
Db       3061 TCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATT 3120

Qy       3121 GGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCA 3180
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Qy       3181 CGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTGT 3240
Db       3181 CGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTCT 3240

Qy       3241 CGGACTCGGAGTACCAGTTCCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTC 3300
Db       3241 CGGACTCGGAGTACCAGTTGCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTC 3300

Qy       3301 CGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCA 3360
Db       3301 CGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCA 3360

Qy       3361 GCCAGGCAGTGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGA 3420
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Qy       3421 GAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCT 3480
Db       3421 GAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCT 3480

Qy       3481 ACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATT 3540
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Qy       3541 ACCTGAACAGAACTCACAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCC 3600
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Qy       3601 GTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACC 3660
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Db       3601 GGGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACC 3660

Qy       3661 GGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTG 3720
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Qy       3721 GTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGG 3780
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Qy       3781 CCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAA 3840
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Db       3781 CCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAA 3840

Qy       3841 AGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGG 3900
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Qy       3961 AGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAA 4020
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Qy       4081 CGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTC 4140
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Qy       4141 CTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTA 4200
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Qy       4201 CAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAAT 4260
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Qy       4261 GGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACT 4320
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Qy       4321 ATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTC 4380
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Qy       4381 GCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCG 4440
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Qy       4441 GTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCACCATA 4500
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Qy       4621 TCTGCGGACCTTTGGTCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGC 4680
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Qy       4681 CAA 4683
             |||
Db       4681 CAA 4683
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RESULT 4
AAD00772
ID   AAD00772 standard; DNA; 4718 BP.
XX
AC   AAD00772;
XX
DT   08-SEP-2000  (first entry)
XX
DE   Adeno-associated virus serotype 1 DNA.
XX
KW   Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein;
KW   cap protein; recombinant viral vector; gene delivery; gene therapy;
KW   vaccine; transgene; ss.
XX
OS   Adeno associated virus serotype 1.
XX
FH   Key             Location/Qualifiers
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FT                   /label= 5'_ITR
FT                   /note= "Inverted terminal repeat which is capable of
FT                   forming T-shaped hairpin structure"
FT   protein_bind    89. .110
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FT   misc_feature    882. .883
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FT                   /note= "P19 RNA"
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FT                   /*tag=  o
FT                   /product= "Rep 40"
FT                   /function= "regulates replication and integration of AAV
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FT                   /note= "The coding region is interrupted by intron"
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FT                   /function= "regulates replication and integration of AAV
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FT                   DNA into host cell's chromosome"
FT   TATA_signal     1836. .1841
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FT                   /label= P40_TATA-BOX
FT   misc_feature    1875. .1876
FT                   /*tag=  q
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FT   intron          1924. .2220
FT                   /*tag=  k
FT                   /note= "This region interrupts the coding sequence of Rep
FT                   68 and Rep 40"
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FT                   /*tag=  r
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FT                   /note= "Capsid protein"
FT   CDS             2634. .4433
FT                   /*tag=  s
FT                   /product= "VP2 protein"
FT                   /note= "Capsid protein"
FT                   /partial
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FT                   /*tag=  t
FT                   /product= "VP3 protein"
FT                   /note= "Capsid protein"
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FT                   /*tag=  u
FT   repeat_unit     4576. .4718
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FT                   forming T-shaped hairpin structure"
XX
PN   WO200028061-A2.
XX
PD   18-MAY-2000.
XX
PF   02-NOV-1999;   99WO-US025694.
XX
PR   05-NOV-1998;   98US-0107114P.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Wilson JM,  Xiao W;
XX
DR   WPI; 2000-376571/32.
DR   P-PSDB; AAY71161, AAY71164, AAY71165, AAY71166, AAY71167, AAY71168,
DR   AAY71169.
XX
PT   Novel adeno-associated virus serotype 1 polynucleotide useful for
PT   preparation of medicament for delivery of a transgene to a host.
XX
PS   Claim 1; Fig 1; 108pp; English.
XX
CC   The present sequence is an adeno-associated virus serotype 1 (AAV-1) DNA
CC   characterised by two inverted terminal repeats (ITR) and open reading
CC   frames for rep and capsid (cap) proteins. The rep reading frame encodes
CC   four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading
CC   frame encodes three structural proteins, VP1, VP2 and VP3. The AAV-1
CC   sequence or its fragments particularly ITRs, rep and cap coding regions,
CC   are useful in production of recombinant viral vectors for gene delivery.
CC   These vectors can be used as gene therapy vectors, vaccine vectors or
CC   antisense delivery vectors. The AAV-1 does not induce the formation of
CC   neutralising antibodies specific to any serotype of AAV hence is useful
CC   for transforming host cells, and in the preparation of a medicament for
CC   the delivery of transgene to a host
XX
SQ   Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;

  Query Match             90.8%;  Score 4253.2;  DB 3;  Length 4718;
  Best Local Similarity   94.7%;  Pred. No. 0;
  Matches 4471;  Conservative    0;  Mismatches  208;  Indels   43;  Gaps    5;

Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
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Db          1 TTGCCCACTCCCTCTCTGCGCGCTCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGC 60

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120

Db         61 AGACGGCAGAGCTCTGCTCTGCCGGCCCCACCGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120

Qy        121 GCCAACTCCATCACTAGGGGT----------------TCCTGGAGGGGTGGAGTCGTGA 163

Db        121 GGCAACTCCATCACTAGGGGTAATCGCGAAGCGCCTCCCACGCTGCCGCGTCAGCGCTGA 180

Qy        164 CGTGAATTACGTCATAGGGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTG-TTTTGC 222

Db        181 CGTAAATTACGTCATAGGG---GAGTGGTCCTGTATTAGCTGTCACGTGAGTGCTTTTGC 237

Qy        223 GACATTTTGCGACACCATGTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGT 282

Db        238 GACATTTTGCGACACCACGTGGCCATTTAGGGTATATATGGCCGAGTGAGCGAGCAGGAT 297

Qy        283 CTCCATTTTGAAGCGGGAGGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGT 342

Db        298 CTCCATTTTGACCGCGAAATTTGAACGAGCAGCAGCCATGCCGGGCTTCTACGAGATCGT 357

Qy        343 GATTAAGGTCCCCAGCGACCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAA 402

Db        358 GATCAAGGTGCCGAGCGACCTGGACGAGCACCTGCCGGGCATTTCTGACTCGTTTGTGAG 417

Qy        403 CTGGGTGGCCGAGAAGGAATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGAT 462

Db        418 CTGGGTGGCCGAGAAGGAATGGGAGCTGCCCCCGGATTCTGACATGGATCTGAATCTGAT 477

Qy        463 TGAGCAGGCACCCCTGACCGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCG 522

Db        478 TGAGCAGGCACCCCTGACCGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCAATGGCG 537

Qy        523 CCGCGTGAGTAAGGCCCCGGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTA 582

Db        538 CCGCGTGAGTAAGGCCCCGGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTA 597

Qy        583 CTTCCACCTCCATATTCTGGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTT 642

Db        598 CTTCCACCTCCATATTCTGGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTT 657

Qy        643 CCTGAGTCAGATTAGCGACAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCT 702

Db        658 CCTGAGTCAGATTAGGGACAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCT 717

Qy        703 GCCCAACTGGTTCGCGGTGACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGT 762

Db        718 GCCCAACTGGTTCGCGGTGACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGT 777

Qy        763 GGACGAGTGCTACATCCCCAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGC 822

Db        778 GGACGAGTGCTACATCCCCAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGC 837

Qy        823 GTGGACTAACATGGAGGAGTATATAAGCGCGTGTTTAAACCTGGCCGAGCGCAAACGGCT 882

Db        838 GTGGACTAACATGGAGGAGTATATAAGCGCCTGTTTGAACCTGGCCGAGCGCAAACGGCT 897

Qy        883 CGTGGCGCACGACCTGACCCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAA 942

Db        898 CGTGGCGCAGCACCTGACCCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGAA 957

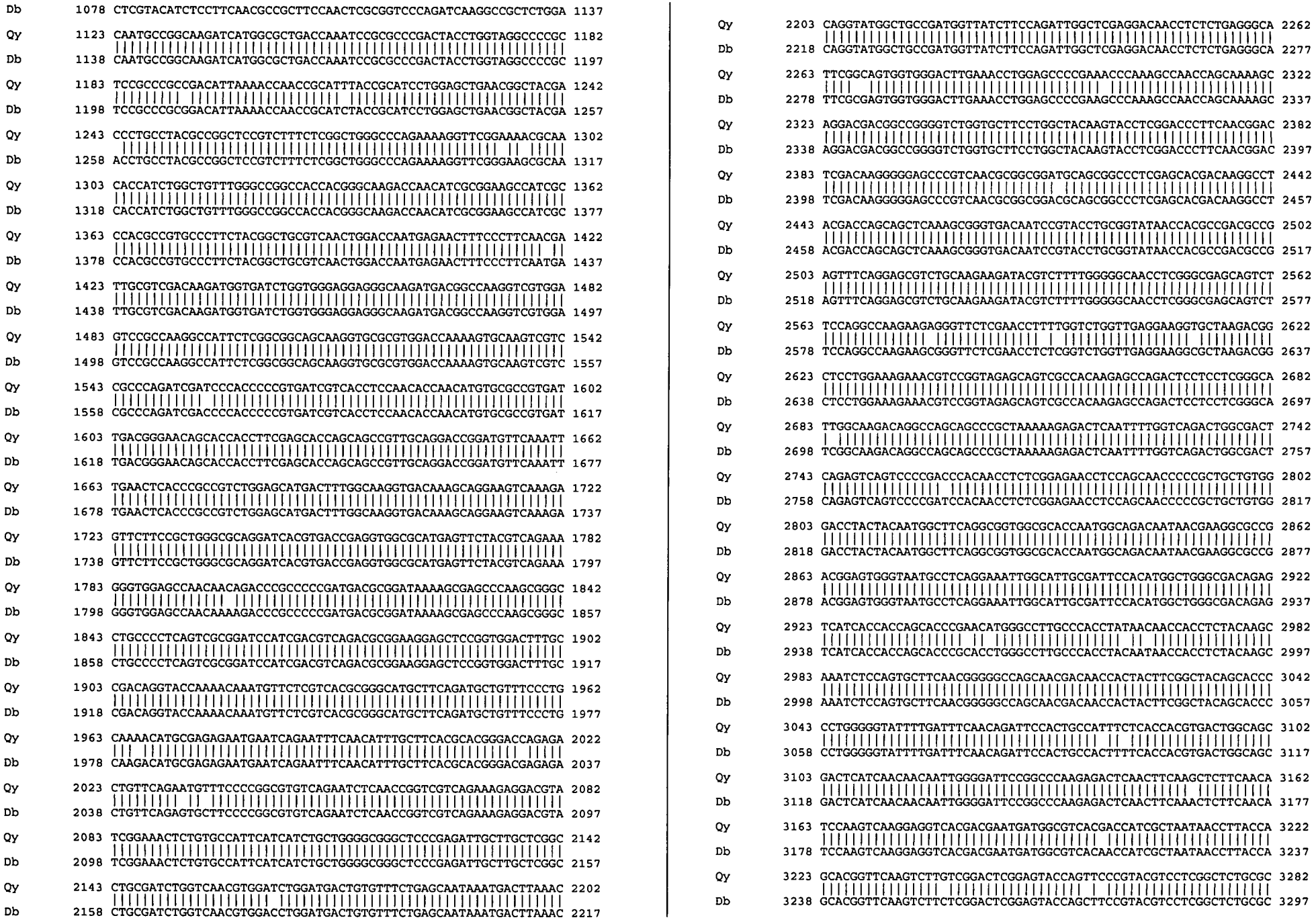
Qy        943 CCCCAATTCTGACGCGCCTGTCATCCGGTCAAAAACCTCCGCACGCTACATGGAGCTGGT 1002

Db        958 CCCCAATTCTGACGCGCCTGTCATCCGGTCAAAAACCTCCGCGCGCTACATGGAGCTGGT 1017

Qy       1003 CGGGTGGCTGGTGGACCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGC 1062

Db       1018 CGGGTGGCTGGTGGACCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGGC 1077

Qy       1063 CTCGTACATCTCCTTCAACGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGA 1122
```


Db 1078 CTCGTACATCTCCTTCAACGCCGCTTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGA 1137
Qy 1123 CAATGCCGGCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGC 1182
Db 1138 CAATGCCGGCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCGC 1197
Qy 1183 TCCGCCCGCCGACATTAAAACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGA 1242
Db 1198 TCCGCCCGCGGACATTAAAACCAACCGCATCTACCGCATCCTGGAGCTGAACGGCTACGA 1257
Qy 1243 CCCTGCCTACGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAA 1302
Db 1258 ACCTGCCTACGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGGAAGCGCAA 1317
Qy 1303 CACCATCTGGCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGC 1362
Db 1318 CACCATCTGGCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGC 1377
Qy 1363 CCACGCCGTGCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGA 1422
Db 1378 CCACGCCGTGCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAATGA 1437
Qy 1423 TTGCGTCGACAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGA 1482
Db 1438 TTGCGTCGACAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGA 1497
Qy 1483 GTCCGCCAAGGCCATTCTCGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTC 1542
Db 1498 GTCCGCCAAGGCCATTCTCGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTC 1557
Qy 1543 CGCCCAGATCGATCCCACCCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGAT 1602
Db 1558 CGCCCAGATCGACCCCACCCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGAT 1617
Qy 1603 TGACGGGAACAGCACCACCTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATT 1662
Db 1618 TGACGGGAACAGCACCACCTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATT 1677
Qy 1663 TGAACTCACCCGCCGTCTGGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGA 1722
Db 1678 TGAACTCACCCGCCGTCTGGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGA 1737
Qy 1723 GTTCTTCCGCTGGGCGCAGGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAA 1782
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Qy 1783 GGGTGGAGCCAACAACAGACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGC 1842
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Qy 1903 CGACAGGTACCAAAACAAATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTG 1962
Db 1918 CGACAGGTACCAAAACAAATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTG 1977
Qy 1963 CAAAACATGCGAGAGAATGAATCAGAATTTCAACATTTGCTTCACGCACGGGACCAGAGA 2022
Db 1978 CAAGACATGCGAGAGAATGAATCAGAATTTCAACATTTGCTTCACGCACGGGACGAGAGA 2037
Qy 2023 CTGTTCAGAATGTTTCCCCGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTA 2082
Db 2038 CTGTTCAGAGTGCTTCCCCGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTA 2097
Qy 2083 TCGGAAACTCTGTGCCATTCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGC 2142
Db 2098 TCGGAAACTCTGTGCCATTCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGC 2157
Qy 2143 CTGCGATCTGGTCAACGTGGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAAC 2202
Db 2158 CTGCGATCTGGTCAACGTGGACCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAAC 2217
Qy 2203 CAGGTATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCA 2262
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Qy 2263 TTCGGCAGTGGTGGGACTTGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGC 2322
Db 2278 TTCGCGAGTGGTGGGACTTGAAACCTGGAGCCCCGAAGCCCAAAGCCAACCAGCAAAAGC 2337
Qy 2323 AGGACGACGGCCGGGGTCTGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGAC 2382
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Qy 2383 TCGACAAGGGGGAGCCCGTCAACGCGGCGGATGCAGCGGCCCTCGAGCACGACAAGGCCT 2442
Db 2398 TCGACAAGGGGGAGCCCGTCAACGCGGCGGACGCAGCGGCCCTCGAGCACGACAAGGCCT 2457
Qy 2443 ACGACCAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCG 2502
Db 2458 ACGACCAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCGGTATAACCACGCCGACGCCG 2517
Qy 2503 AGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCT 2562
Db 2518 AGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCT 2577
Qy 2563 TCCAGGCCAAGAAGAGGGTTCTCGAACCTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGG 2622
Db 2578 TCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGTCTGGTTGAGGAAGGCGCTAAGACGG 2637
Qy 2623 CTCCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCA 2682
Db 2638 CTCCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCA 2697
Qy 2683 TTGGCAAGACAGGCCAGCAGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACT 2742
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Qy 2983 AAATCTCCAGTGCTTCAACGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCC 3042
Db 2998 AAATCTCCAGTGCTTCAACGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCC 3057
Qy 3043 CCTGGGGGTATTTTGATTTCAACAGATTCCACTGCCATTTCTCACCACGTGACTGGCAGC 3102
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Qy 3163 TCCAAGTCAAGGAGGTCACGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCA 3222
Db 3178 TCCAAGTCAAGGAGGTCACGACGAATGATGGCGTCACAACCATCGCTAATAACCTTACCA 3237
Qy 3223 GCACGGTTCAAGTCTTGTCGGACTCGGAGTACCAGTTCCCGTACGTCCTCGGCTCTGCGC 3282
Db 3238 GCACGGTTCAAGTCTTCTCGGACTCGGAGTACCAGCTTCCGTACGTCCTCGGCTCTGCGC 3297

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Qy       3283 ACCAGGGCTGCCTCCCTCCGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACC 3342
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       3298 ACCAGGGCTGCCTCCCTCCGTTCCCGGCGGACGTGTTCATGATTCCGCAATACGGCTACC 3357

Qy       3343 TAACGCTCAACAATGGCAGCCAGGCAGTGGGACGCTCATCCTTTTACTGCCTGGAATATT 3402
             | |||||||||||||||||| || |||||||| |||||||||||||||||||||||||||
Db       3358 TGACGCTCAACAATGGCAGCCAAGCCGTGGGACGTTCATCCTTTTACTGCCTGGAATATT 3417

Qy       3403 TCCCATCGCAGATGCTGAGAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACG 3462
             ||||  || |||||||||||||||||||| |||||||||||||||||||||| ||||| |
Db       3418 TCCCTTCTCAGATGCTGAGAACGGGCAACAACTTTACCTTCAGCTACACCTTTGAGGAAG 3477

Qy       3463 TGCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCA 3522
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3478 TGCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCA 3537

Qy       3523 TCGACCAGTACCTGTATTACCTGAACAGAACTCACAATCAGTCCGGAAGTGCCCAAAACA 3582
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Qy       3583 AGGACTTGCTGTTTAGCCGTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGC 3642
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Db       3598 AGGACTTGCTGTTTAGCCGTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGC 3657

Qy       3643 TACCTGGACCCTGTTACCGGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACA 3702
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Qy       3703 GCAACTTTACCTGGACTGGTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCA 3762
             ||||  |||||||||||||||||||||||||||||||||  |||||||||||||  || ||||
Db       3718 GCAATTTTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGGCGTGAATCCATCATCA 3777

Qy       3763 ACCCTGGCACTGCTATGGCCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCG 3822
             |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       3778 ACCCTGGCACTGCTATGGCCTCACACAAAGACGACGAAGACAAGTTCTTTCCCATGAGCG 3837

Qy       3823 GTGTCATGATTTTTGGAAAGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCA 3882
             ||||||||||||||||||  |||||||||||||||||||||||||||||||||||||||||
Db       3838 GTGTCATGATTTTTGGAAAAGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCA 3897

Qy       3883 TGATCACAGACGAAGAGGAAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGA 3942
             ||||  |||||||||||||||||  |||||||||||||  |||||||||||||||||||||||
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Qy       3943 CTGTGGCAGTCAATCTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTA 4002
             | ||||||||||||  |||||||||||||||||||||||||||||||||||||||||  ||
Db       3958 CCGTGGCAGTCAATTTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGCTA 4017

Qy       4003 TGGGAGCCTTACCTGGAATGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTT 4062
             |||||||  |||||||| ||||||||||||||  |||||||| |||||||||||||  ||||
Db       4018 TGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTT 4077

Qy       4063 GGGCCAAAATTCCTCACACGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTG 4122
             ||||||||||||||||||  |||||||||||||||||||||||||||  ||||||||||||||
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Qy       4123 GACTTAAGCACCCGCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTC 4182
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Qy       4183 CGGCAGAGTTTTCGGCTACAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAG 4242
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Qy       4243 TGAGCGTGGAGATTGAATGGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAG 4302
             ||||  |||||  ||||||||||||||||||||||||||||||||  ||||||||||||||||
Db       4258 TGAGTGTGGAAATTGAATGGGAGCTGCAGAAAGAAAACAGCAAGCGCTGGAATCCCGAAG 4317

Qy       4303 TGCAGTATACATCTAACTATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATG 4362
             |||||||  |||||  ||  |||||||||||||||||||||||||  ||||||||||||||||
Db       4318 TGCAGTACACATCCAATTATGCAAAATCTGCCAACGTTGATTTTACTGTGGACAACAATG 4377

Qy       4363 GACTTTATACTGAGCCTCGCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGT 4422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4378 GACTTTATACTGAGCCTCGCCCCATTGGCACCCGTTACCTTACCCGTCCCCTGTAATTAC 4437

Qy       4423 GTGTTAATCAATAAACCGGTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTA 4482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4438 GTGTTAATCAATAAACCGGTTGATTCGTTTCAGTTGAACTTTGGTCTCCTGTCCTTCTTA 4497

Qy       4483 TCTTATCTGGTCACCATAGCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGA-- 4540
             |||||||  |||  |||||  |   |  | ||||||||||||||||||  ||||||||||||||
Db       4498 TCTTATC-GGTTACCATGGTTATAGCTTACACATTAACTGCTTGGTTGCGCTTCGCGATA 4556

Qy       4541 ------------------ATACCCCTAGTGATGGAGTTGCCCACTCCCTCTATGCGCGC 4581
                                  |||||||||||||||||||||||||||||||  |||||||
Db       4557 AAAGACTTACGTCATCGGGTTACCCCTAGTGATGGAGTTGCCCACTCCCTCTCTGCGCGC 4616

Qy       4582 TCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCGTCTGCGGACCTTTGGTCCGCA 4641
             ||||||||||||||||||  || ||  ||  || || ||  | |  || ||  || ||  || ||
Db       4617 TCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGCAGACGGCAGAGCTCTGCTCTGCC 4676

Qy       4642 GGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGCCAA 4683
             |||||||||||||||||||||||||  ||||||||||  |||
Db       4677 GGCCCCACCGAGCGAGCGAGCGCGCAGAGAGGGAGTGGGCAA 4718
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RESULT 5
ADE76507
ID ADE76507 standard; DNA; 4718 BP.
XX
AC ADE76507;
XX
DT 29-JAN-2004 (first entry)
XX
DE Adeno-associated virus (AAV) related DNA, SEQ ID No 6.
XX
KW adeno-associated virus; AAV; cytostatic; antipsoriatic; antirheumatic;
KW antiarthritic; neuroprotective; antidiabetic; antithyroid;
KW dermatological; antiinflammatory; gene therapy; vaccine;
KW hyperproliferative; cancer; psoriasis; autoimmune disease;
KW rheumatoid arthritis; multiple sclerosis; diabetes;
KW autoimmune thyroiditis; scleroderma; Crohn's disease; gene; ds.
XX
OS Adeno-associated virus 1.
XX
PN EP1310571-A2.
XX
PD 14-MAY-2003.
XX
PF 12-NOV-2002; 2002EP-00257826.
XX
PR 13-NOV-2001; 2001US-0350607P.
PR 17-DEC-2001; 2001US-0341117P.
PR 01-MAY-2002; 2002US-0377066P.
PR 05-JUN-2002; 2002US-0386675P.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Gao G, Wilson JM, Alvira M;
XX
DR WPI; 2003-450984/43.
XX
PT Detecting adeno-associated virus sequences in a sample, useful for e.g.
PT preventing or treating hyperproliferative or autoimmune diseases,
PT comprises subjecting a sample having a DNA to amplification via
PT polymerase chain reaction.
XX
PS Claim 14; SEQ ID NO 6; 419pp; English.
XX
CC The invention relates to a novel method for detecting adeno-associated
CC virus (AAV) sequences in a sample, which comprises subjecting a sample
CC containing a DNA to amplification via a polymerase chain reaction (PCR).
CC The AAV sequence have the following activities: cytostatic,
CC antipsoriatic, antirheumatic, antiarthritic, neuroprotective,
CC antidiabetic, antithyroid, dermatological, and antiinflammatory. The AAV

CC sequence can be used in gene therapy or as part of a vaccine to treat
CC disorders. The method is useful in detecting and/or identifying AAV
CC sequences and isolating novel sequences that are identified. The
CC sequences may be used e.g. for preventing or treating hyperproliferative
CC conditions such as cancers and psoriasis, and other autoimmune diseases
CC like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune
CC thyroiditis, scleroderma or Crohn's disease. This polynucleotide sequence
CC represents an AAV related DNA sequence of the invention.
XX
SQ Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;

Query Match 90.8%; Score 4253.2; DB 10; Length 4718;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 4471; Conservative 0; Mismatches 208; Indels 43; Gaps 5;

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Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
              ||| |||||||||||||||||||||||||||||||  || |||| |  ||||||||||  |
Db          1 TTGCCCACTCCCTCTCTGCGCGCTCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGC 60

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
                |||| | | ||| ||| | | ||||| ||  |||||||||||||||||||||||||||||
Db         61 AGACGGCAGAGCTCTGCTCTGCCGGCCCCACCGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120

Qy        121 GCCAACTCCATCACTAGGGGT----------------TCCTGGAGGGGTGGAGTCGTGA 163
              | ||||||||||||||||||                |       |    ||  |||
Db        121 GGCAACTCCATCACTAGGGGTAATCGCGAAGCGCCTCCCACGCTGCCGCGTCAGCGCTGA 180

Qy        164 CGTGAATTACGTCATAGGGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTG-TTTTGC 222
              ||| ||||||||||||||   | | ||||||||||||  ||||||||||| ||||||
Db        181 CGTAAATTACGTCATAGGG---GAGTGGTCCTGTATTAGCTGTCACGTGAGTGCTTTTGC 237

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Qy        583 CTTCCACCTCCATATTCTGGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCTT 642
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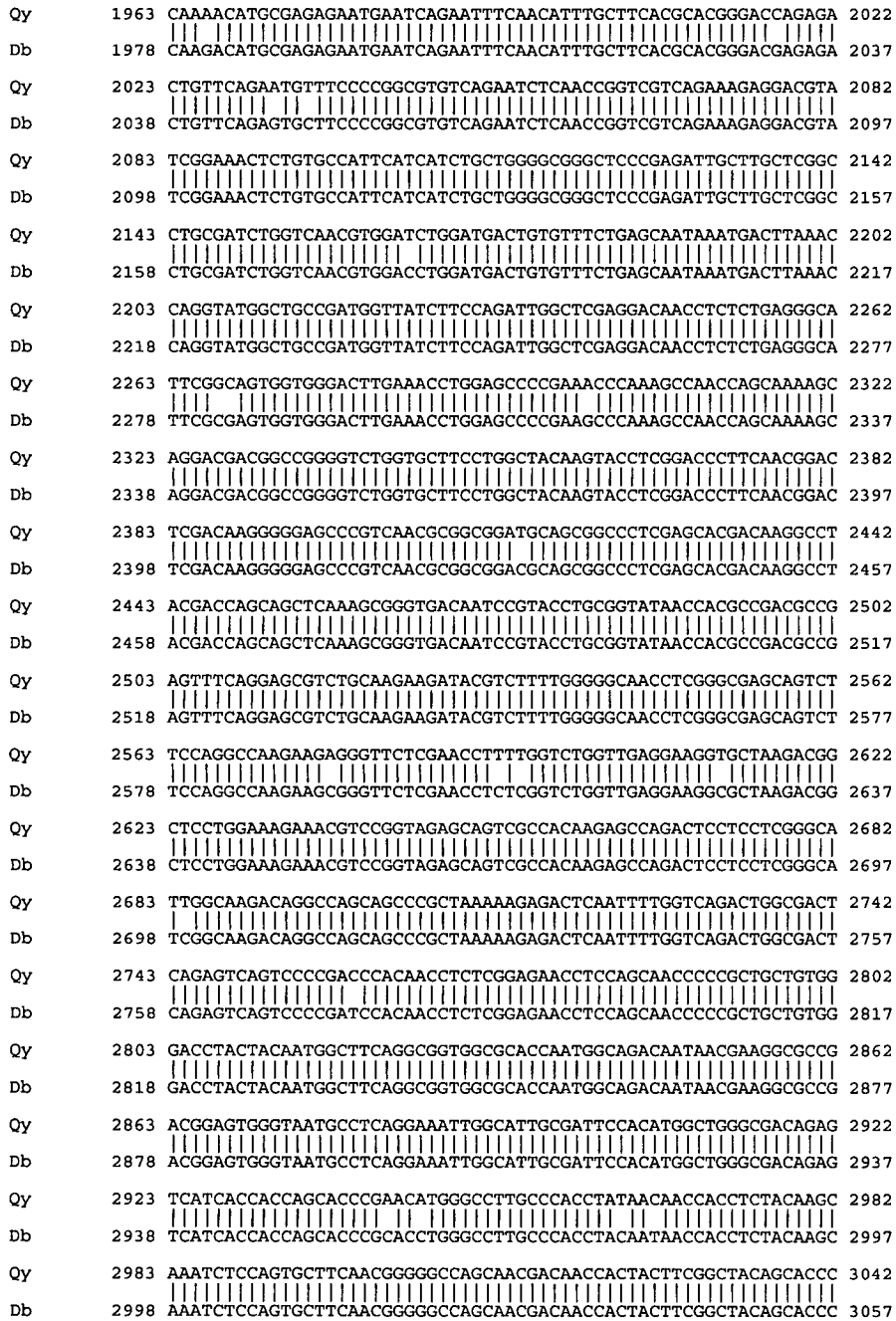
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RESULT 6
ADL13984
ID ADL13984 standard; DNA; 4718 BP.
XX
AC ADL13984;
XX
DT 06-MAY-2004 (first entry)
XX
DE Adeno-associated virus serotype 1 complete DNA.
XX
KW ss; cytostatic; neuroprotective; antiinflammatory; gene therapy;
KW expression construct; adeno-associated virus;
KW integration efficiency element; inverted terminal repeat; integration;
KW chromosome; cancer; lymphoma; leukemia; multiple myeloma; neuroblastoma;
KW retinoblastoma; inflammatory disease; arthritis;
KW neurodegenerative disease.
XX
OS Adeno-associated virus 1.
XX
PN WO2003087334-A2.
XX
PD 23-OCT-2003.
XX
PF 09-APR-2003; 2003WO-US011191.
XX
PR 09-APR-2002; 2002US-0371044P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Falck-Pedersen ES, Philpott N;
XX
DR WPI; 2003-833723/77.
XX
PT New expression construct comprising a nucleic acid sequence encoding an
PT adeno-associated virus integration efficiency element, useful for
PT treating cancer e.g. lung cancer or colon cancer or inflammatory disease
PT e.g. arthritis.
XX
PS Disclosure; SEQ ID NO 3; 62pp; English.
XX
CC The invention relates to an expression construct comprising a nucleic
CC acid sequence encoding an adeno-associated virus integration efficiency
CC element (AAV IEE), which is devoid of AAV inverted terminal repeats (AAV
CC ITRs) and site-specifically integrates into a host cell chromosome when
CC provided to the host cell in conjunction with an AAV Rep protein. The
CC expression construct can be used as a therapeutic factor for treating a
CC mammal for a pathologic state which is cancer, including lung cancer,
CC colon cancer, renal cancer, anal cancer, bile duct cancer, bladder
CC cancer, bone cancer, brain cancer, spinal chord cancer, breast cancer,
CC cervical cancer, lymphoma, endometrial cancer, esophageal cancer,
CC gallbladder cancer, gastrointestinal cancer, laryngeal cancer, leukemia,
CC liver cancer, multiple myeloma, neuroblastoma, ovarian cancer, pancreatic
CC cancer, prostatic cancer, retinoblastoma, skin cancer, stomach cancer,
CC testicular cancer, thymus cancer or thyroid cancer. Other pathologic
CC state includes inflammatory disease (arthritis), neurodegenerative
CC disease, a disease of an organ attributed to the presence of increased or
CC decreased level of a particular gene product(s). This sequence
CC corresponds to the AAV serotype 1 complete DNA including the IEE
CC sequence.
XX
SQ Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;

Query Match 90.8%; Score 4253.2; DB 10; Length 4718;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 4471; Conservative 0; Mismatches 208; Indels 43; Gaps 5;

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Db         61 AGACGGCAGAGCTCTGCTCTGCCGGCCCCACCGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120

Qy        121 GCCAACTCCATCACTAGGGGT----------------TCCTGGAGGGGTGGAGTCGTGA 163

Db        121 GGCAACTCCATCACTAGGGGTAATCGCGAAGCGCCTCCCACGCTGCCGCGTCAGCGCTGA 180

Qy        164 CGTGAATTACGTCATAGGGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTG-TTTTGC 222

Db        181 CGTAAATTACGTCATAGGG---GAGTGGTCCTGTATTAGCTGTCACGTGAGTGCTTTTGC 237

Qy        223 GACATTTTGCGACACCATGTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGT 282

Db        238 GACATTTTGCGACACCACGTGGCCATTTAGGGTATATATGGCCGAGTGAGCGAGCAGGAT 297

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Db        298 CTCCATTTTGACCGCGAAATTTGAACGAGCAGCAGCCATGCCGGGCTTCTACGAGATCGT 357

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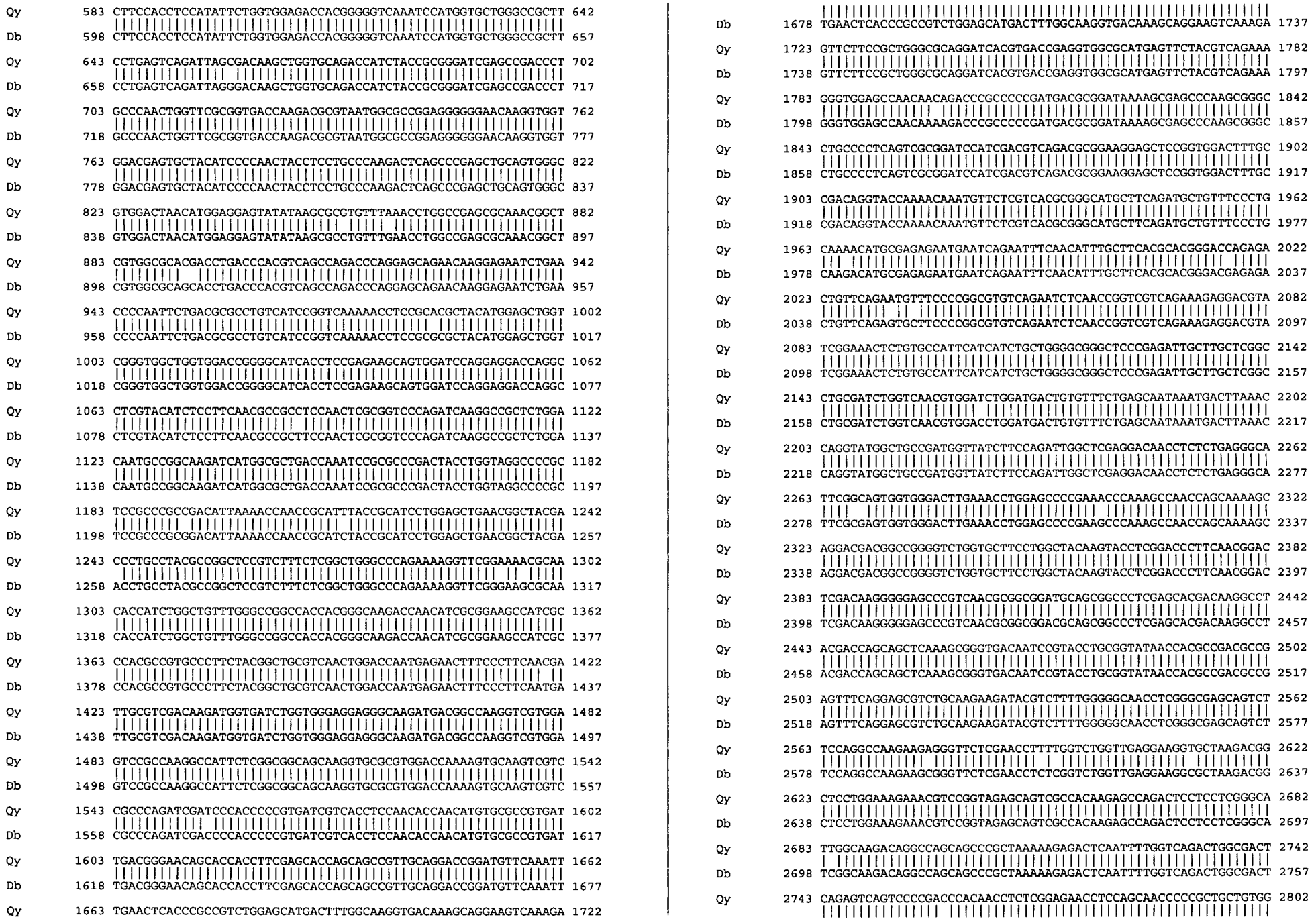
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Db 718 GCCCAACTGGTTCGCGGTGACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGGT 777
Qy 763 GGACGAGTGCTACATCCCCAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGC 822
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Qy 1183 TCCGCCCGCCGACATTAAAACCAACCGCATTTACCGCATCCTGGAGCTGAACGGCTACGA 1242
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Qy 1303 CACCATCTGGCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGC 1362
Db 1318 CACCATCTGGCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCGC 1377
Qy 1363 CCACGCCGTGCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAACGA 1422
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Qy 1423 TTGCGTCGACAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGA 1482
Db 1438 TTGCGTCGACAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGA 1497
Qy 1483 GTCCGCCAAGGCCATTCTCGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTC 1542
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Qy 2683 TTGGCAAGACAGGCCAGCAGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGCGACT 2742
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Qy 2743 CAGAGTCAGTCCCCGACCCACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCTGTGG 2802

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Qy       3343 TAACGCTCAACAATGGCAGCCAGGCAGTGGGACGCTCATCCTTTTACTGCCTGGAATATT 3402
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Qy       3403 TCCCATCGCAGATGCTGAGAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACG 3462
Db       3418 TCCCTTCTCAGATGCTGAGAACGGGCAACAACTTTACCTTCAGCTACACCTTTGAGGAAG 3477
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Db       3478 TGCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCA 3537
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Qy       4183 CGGCAGAGTTTTCGGCTACAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAG 4242
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Qy       4423 GTGTTAATCAATAAACCGGTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTA 4482
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Qy       4541 -------------------ATACCCCTAGTGATGGAGTTGCCCACTCCCTCTATGCGCGC 4581
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Qy       4642 GGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGCCAA 4683
Db       4677 GGCCCCACCGAGCGAGCGAGCGCGCAGAGAGGGAGTGGGCAA 4718
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RESULT 7
ADG39758
ID ADG39758 standard; DNA; 4718 BP.
XX
AC ADG39758;
XX
DT 11-MAR-2004 (first entry)
XX
DE AAV-1 genomic DNA sequence SEQ ID NO:20.
XX
KW parvovirus; rep; cap; DNA binding domain; capsid interacting domain;
KW recombinant hybrid parvovirus particle;
KW recombinant adeno-associated virus; rAAV; AAV; vaccine; gene therapy;
KW gene; ds.
XX

OS Adeno-associated virus 1.
XX
PN WO2003104392-A2.
XX
PD 18-DEC-2003.
XX
PF 02-DEC-2002; 2002WO-US038423.
XX
PR 18-DEC-2001; 2001US-0341919P.
XX
PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Samulski RJ, Rabinowitz JE;
XX
DR WPI; 2004-062324/06.
XX
PT New polynucleotides comprising parvovirus rep coding sequences and
PT parvovirus cap coding sequences, useful in producing higher stocks of
PT hybrid parvovirus vectors for delivering therapeutic nucleic acids to a
PT subject.
XX
PS Disclosure; SEQ ID NO 20; 115pp; English.
XX
CC The present invention describes a polynucleotide (I), comprising
CC parvovirus rep coding sequences and parvovirus cap coding sequences. The
CC rep coding sequences encodes a DNA binding domain from a first
CC parvovirus, and a capsid interacting domain from a parvovirus different
CC from the first parvovirus. The cap coding sequence comprises sequences
CC from the different parvovirus. Also described: (1) a vector comprising
CC (I); (2) a cell comprising (I), or parvovirus rep coding sequences and
CC parvovirus cap coding sequences, where the rep coding sequences encode a
CC DNA binding domain from a first parvovirus and a capsid interacting
CC domain from a parvovirus different from the first parvovirus, the cap
CC coding sequences comprise sequences from the different parvovirus, and
CC the rep coding sequences are stably integrated into the genome of the
CC cell; and (3) producing a recombinant hybrid parvovirus particle or adeno
CC -associated virus (rAAV) particle. (I) can be used in vaccines, and in
CC gene therapy. The polynucleotide (I) can be used in producing higher
CC stocks of hybrid parvoviruses or parvovirus vectors, which may be used in
CC the delivery of nucleic acids having biological effect to treat or
CC ameliorate the symptoms associated with any disorder related to gene
CC expression. The polynucleotide may be used to produce a parvovirus vector
CC to express an immunogenic polypeptide in a subject, e.g. for vaccination.
CC The parvovirus vector may also be used to provide an antisense nucleic
CC acid to a cell in vitro or in vivo, or in diagnostic and screening
CC methods. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 4718 BP; 1121 A; 1393 C; 1273 G; 931 T; 0 U; 0 Other;

Query Match 90.8%; Score 4253.2; DB 12; Length 4718;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 4471; Conservative 0; Mismatches 208; Indels 43; Gaps 5;

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Db          1 TTGCCCACTCCCTCTCTGCGCGCTCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGC 60

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
               |||| | | ||| ||| | | ||||| ||  ||||||||||||||||||||||||||||
Db         61 AGACGGCAGAGCTCTGCTCTGCCGGCCCCACCGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120

Qy        121 GCCAACTCCATCACTAGGGGT----------------TCCTGGAGGGGTGGAGTCGTGA 163
              | ||||||||||||||||||                |     |   ||   |||
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Qy        164 CGTGAATTACGTCATAGGGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTG-TTTTGC 222
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Qy        343 GATTAAGGTCCCCAGCGACCTTGACGAGCATCTGCCCGGCATTTCTGACAGCTTTGTGAA 402
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Db        358 GATCAAGGTGCCGAGCGACCTGGACGAGCACCTGCCGGGCATTTCTGACTCGTTTGTGAG 417

Qy        403 CTGGGTGGCCGAGAAGGAATGGGAGTTGCCGCCAGATTCTGACATGGATCTGAATCTGAT 462
              |||||||||||||||||||||||||| |||| || ||||||||||||||||||||||||||
Db        418 CTGGGTGGCCGAGAAGGAATGGGAGCTGCCCCCGGATTCTGACATGGATCTGAATCTGAT 477

Qy        463 TGAGCAGGCACCCCTGACCGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCACTGGCG 522
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
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Qy        523 CCGCGTGAGTAAGGCCCCGGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTA 582
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Qy        643 CCTGAGTCAGATTAGCGACAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCCT 702
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Qy        763 GGACGAGTGCTACATCCCCAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGC 822
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Qy       1063 CTCGTACATCTCCTTCAACGCCGCCTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGGA 1122
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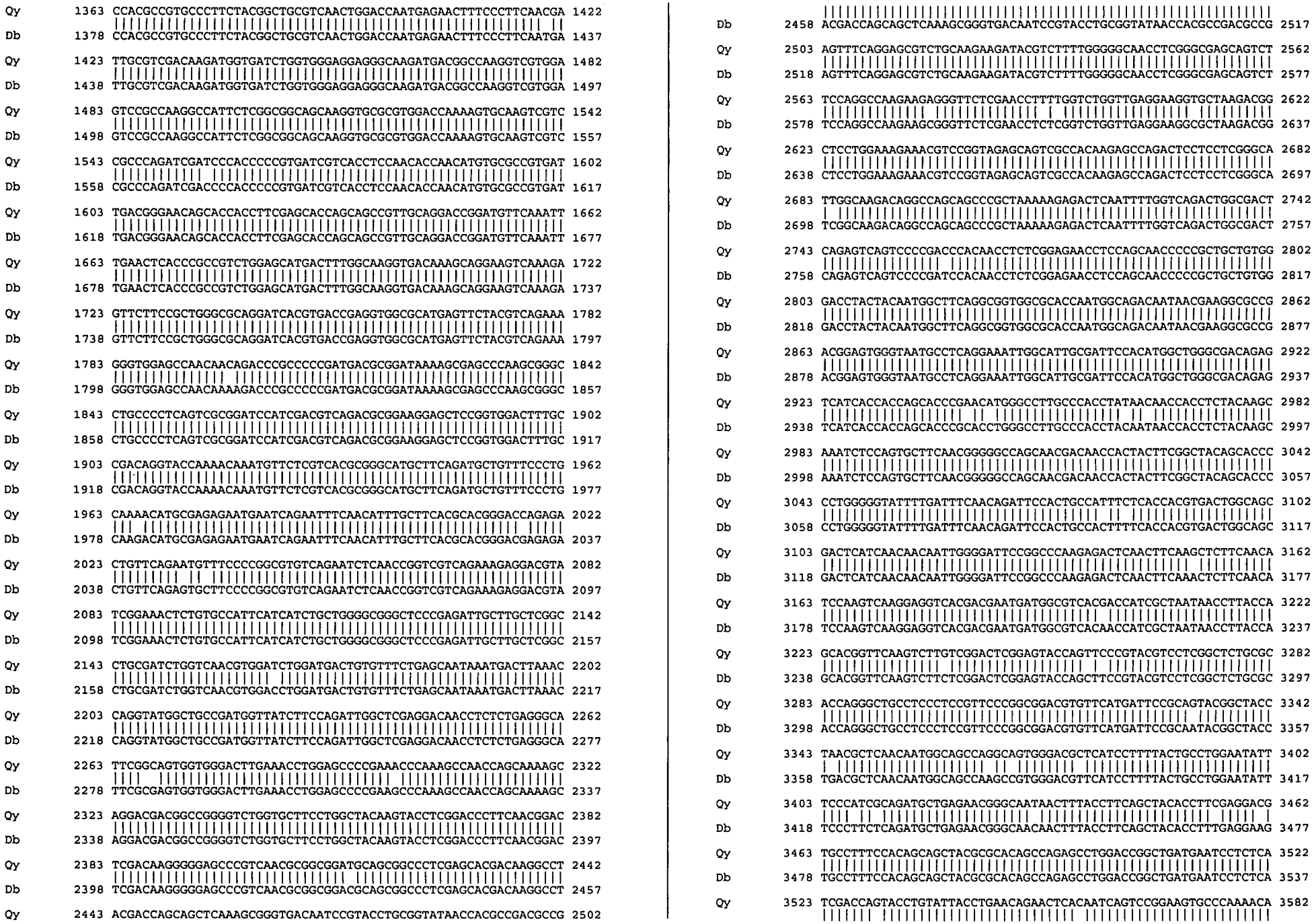
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Qy 1423 TTGCGTCGACAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGA 1482
Db 1438 TTGCGTCGACAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGGA 1497
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Qy 1603 TGACGGGAACAGCACCACCTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATT 1662
Db 1618 TGACGGGAACAGCACCACCTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAATT 1677
Qy 1663 TGAACTCACCCGCCGTCTGGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGA 1722
Db 1678 TGAACTCACCCGCCGTCTGGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGA 1737
Qy 1723 GTTCTTCCGCTGGGCGCAGGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAA 1782
Db 1738 GTTCTTCCGCTGGGCGCAGGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAAA 1797
Qy 1783 GGGTGGAGCCAACAACAGACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGGC 1842
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Qy 1843 CTGCCCCTCAGTCGCGGATCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGC 1902
Db 1858 CTGCCCCTCAGTCGCGGATCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTGC 1917
Qy 1903 CGACAGGTACCAAAACAAATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCTG 1962
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Db 2038 CTGTTCAGAGTGCTTCCCCGGCGTGTCAGAATCTCAACCGGTCGTCAGAAAGAGGACGTA 2097
Qy 2083 TCGGAAACTCTGTGCCATTCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGC 2142
Db 2098 TCGGAAACTCTGTGCCATTCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGC 2157
Qy 2143 CTGCGATCTGGTCAACGTGGATCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAAC 2202
Db 2158 CTGCGATCTGGTCAACGTGGACCTGGATGACTGTGTTTCTGAGCAATAAATGACTTAAAC 2217
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Db 2218 CAGGTATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCA 2277
Qy 2263 TTCGGCAGTGGTGGGACTTGAAACCTGGAGCCCCGAAACCCAAAGCCAACCAGCAAAAGC 2322
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Db 2518 AGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCT 2577
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Db 2578 TCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGTCTGGTTGAGGAAGGCGCTAAGACGG 2637
Qy 2623 CTCCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCA 2682
Db 2638 CTCCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCA 2697
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Db 2818 GACCTACTACAATGGCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGCGCCG 2877
Qy 2863 ACGGAGTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAG 2922
Db 2878 ACGGAGTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGACAGAG 2937
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Db 3058 CCTGGGGGTATTTTGATTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGC 3117
Qy 3103 GACTCATCAACAACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACA 3162
Db 3118 GACTCATCAACAACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAAACTCTTCAACA 3177
Qy 3163 TCCAAGTCAAGGAGGTCACGACGAATGATGGCGTCACGACCATCGCTAATAACCTTACCA 3222
Db 3178 TCCAAGTCAAGGAGGTCACGACGAATGATGGCGTCACAACCATCGCTAATAACCTTACCA 3237
Qy 3223 GCACGGTTCAAGTCTTGTCGGACTCGGAGTACCAGTTCCCGTACGTCCTCGGCTCTGCGC 3282
Db 3238 GCACGGTTCAAGTCTTCTCGGACTCGGAGTACCAGCTTCCGTACGTCCTCGGCTCTGCGC 3297
Qy 3283 ACCAGGGCTGCCTCCCTCCGTTCCCGGCGGACGTGTTCATGATTCCGCAGTACGGCTACC 3342
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Db 3358 TGACGCTCAACAATGGCAGCCAAGCCGTGGGACGTTCATCCTTTTACTGCCTGGAATATT 3417
Qy 3403 TCCCATCGCAGATGCTGAGAACGGGCAATAACTTTACCTTCAGCTACACCTTCGAGGACG 3462
Db 3418 TCCCTTCTCAGATGCTGAGAACGGGCAACAACTTTACCTTCAGCTACACCTTTGAGGAAG 3477
Qy 3463 TGCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCA 3522
Db 3478 TGCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCTCTCA 3537
Qy 3523 TCGACCAGTACCTGTATTACCTGAACAGAACTCACAATCAGTCCGGAAGTGCCCAAAACA 3582

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Db       3538 TCGACCAATACCTGTATTACCTGAACAGAACTCAAAATCAGTCCGGAAGTGCCCAAAACA 3597

Qy       3583 AGGACTTGCTGTTTAGCCGTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGC 3642
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Db       3598 AGGACTTGCTGTTTAGCCGTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGC 3657

Qy       3643 TACCTGGACCCTGTTACCGGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACA 3702
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Db       3658 TACCTGGACCCTGTTATCGGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAACAACA 3717

Qy       3703 GCAACTTTACCTGGACTGGTGCTTCAAAATATAACCTTAATGGGCGTGAATCTATAATCA 3762
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Qy       3763 ACCCTGGCACTGCTATGGCCTCACACAAAGACGACAAAGACAAGTTCTTTCCCATGAGCG 3822
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Qy       3823 GTGTCATGATTTTTGGAAAGGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCA 3882
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Db       3838 GTGTCATGATTTTTGGAAAAGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAATGTCA 3897

Qy       3883 TGATCACAGACGAAGAGGAAATCAAAGCCACTAACCCCGTGGCCACCGAAAGATTTGGGA 3942
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Qy       3943 CTGTGGCAGTCAATCTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGTTA 4002
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Db       3958 CCGTGGCAGTCAATTTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCATGCTA 4017

Qy       4003 TGGGAGCCTTACCTGGAATGGTGTGGCAAGACAGAGACGTATACCTGCAGGGTCCTATTT 4062
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Db       4018 TGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCCATTT 4077

Qy       4063 GGGCCAAAATTCCTCACACGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCTTTG 4122
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Db       4078 GGGCCAAAATTCCTCACACAGATGGACACTTTCACCCGTCTCCTCTTATGGGCGGCTTTG 4137

Qy       4123 GACTTAAGCACCCGCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTC 4182
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Db       4138 GACTCAAGAACCCGCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAATCCTC 4197

Qy       4183 CGGCAGAGTTTTCGGCTACAAAGTTTGCTTCATTCATCACCCAGTATTCCACAGGACAAG 4242
             |||| |||||||| |||||||||||||||||||||||||||||| || ||||||||||||
Db       4198 CGGCGGAGTTTTCAGCTACAAAGTTTGCTTCATTCATCACCCAATACTCCACAGGACAAG 4257

Qy       4243 TGAGCGTGGAGATTGAATGGGAGCTGCAGAAAGAAAACAGCAAACGCTGGAATCCCGAAG 4302
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Db       4258 TGAGTGTGGAAATTGAATGGGAGCTGCAGAAAGAAAACAGCAAGCGCTGGAATCCCGAAG 4317

Qy       4303 TGCAGTATACATCTAACTATGCAAAATCTGCCAACGTTGATTTCACTGTGGACAACAATG 4362
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Qy       4363 GACTTTATACTGAGCCTCGCCCCATTGGCACCCGTTACCTCACCCGTCCCCTGTAATTGT 4422
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Db       4378 GACTTTATACTGAGCCTCGCCCCATTGGCACCCGTTACCTTACCCGTCCCCTGTAATTAC 4437

Qy       4423 GTGTTAATCAATAAACCGGTTAATTCGTGTCAGTTGAACTTTGGTCTCATGTCCTTATTA 4482
             |||||||||||||||||||| |||||| |||||||||||||||||| ||||||| |||
Db       4438 GTGTTAATCAATAAACCGGTTGATTCGTTTCAGTTGAACTTTGGTCTCCTGTCCTTCTTA 4497

Qy       4483 TCTTATCTGGTCACCATAGCAACCGGTTACACATTAACTGCTTAGTTGCGCTTCGCGA-- 4540
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Db       4498 TCTTATC-GGTTACCATGGTTATAGCTTACACATTAACTGCTTGGTTGCGCTTCGCGATA 4556

Qy       4541 ------------------ATACCCCTAGTGATGGAGTTGCCCACTCCCTCTATGCGCGC 4581
                                  |||||||||||||||||||||||||||||||| |||||||
Db       4557 AAAGACTTACGTCATCGGGTTACCCCTAGTGATGGAGTTGCCCACTCCCTCTCTGCGCGC 4616

Qy       4582 TCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCGTCTGCGGACCTTTGGTCCGCA 4641
             |||||||||||||||||| || || || || || || | | || || || || || || ||
Db       4617 TCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGCAGACGGCAGAGCTCTGCTCTGCC 4676
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Qy       4642 GGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGCCAA 4683
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Db       4677 GGCCCCACCGAGCGAGCGAGCGCGCAGAGAGGGAGTGGGCAA 4718
```

RESULT 8
ADW39402
ID ADW39402 standard; DNA; 4239 BP.
XX
AC ADW39402;
XX
DT 24-MAR-2005 (first entry)
XX
DE Adeno-associated virus 2 (AAV2) rep-AAV1 cap fusion DNA - SEQ ID 5.
XX
KW genetically engineered microorganism; vector; rep; cap; ds.
XX
OS Adeno-associated virus 2.
OS Chimeric.
OS Unidentified.
XX
PN CN1461805-A.
XX
PD 17-DEC-2003.
XX
PF 27-MAY-2002; 2002CN-00117965.
XX
PR 27-MAY-2002; 2002CN-00117965.
XX
PA (BENY-) BENYUAN ZHENGYANG GENETIC TECHNOLOGY CO.
XX
PI Wu X, Cao H, Dong X;
XX
DR WPI; 2004-248658/24.
XX
PT Structure of a recombinant herpes simplex virus and its use.
XX
PS Claim 5; SEQ ID NO 5; 102pp; Chinese.
XX
CC The invention relates to a novel recombinant herpes simplex virus (rHSVS)
CC whose genome is respectively inserted by the Adeno-associated virus (AAV)
CC rep gene and cap gene. The AVV genes may be derived from viruses AAV1,
CC AAV2, AAV3, AAV4, AAV5 and AAV6. The methods of the invention may be
CC useful for generating recombinant vectors with high efficiency and no
CC need of reconfiguration. The current sequence is that of the Adeno-
CC associated virus 2 (AAV2) rep-Adeno-associated virus 1 (AAV1) cap fusion
CC DNA (SEQ ID 5) of the invention.
XX
SQ Sequence 4239 BP; 1084 A; 1156 C; 1130 G; 869 T; 0 U; 0 Other;

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  Query Match            81.8%;  Score 3831.4;  DB 13;  Length 4239;
  Best Local Similarity  94.3%;  Pred. No. 0;
  Matches 3997;  Conservative    0;  Mismatches  236;  Indels    4;  Gaps    2;

Qy        191 GTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCATGTGGTCACGC 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCATGTGGTCACGC 65

Qy        251 TGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGAGGTTTGAACG 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 TGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGAGGTTTGAACG 125

Qy        311 CGCAG-CGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGACCTTGACGA 369
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CGCAGCCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGACCTTGACGG 185

Qy        370 GCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGAATGGGAGTT 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGAATGGGAGTT 245

Qy        430 GCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGACCGTGGCCGA 489
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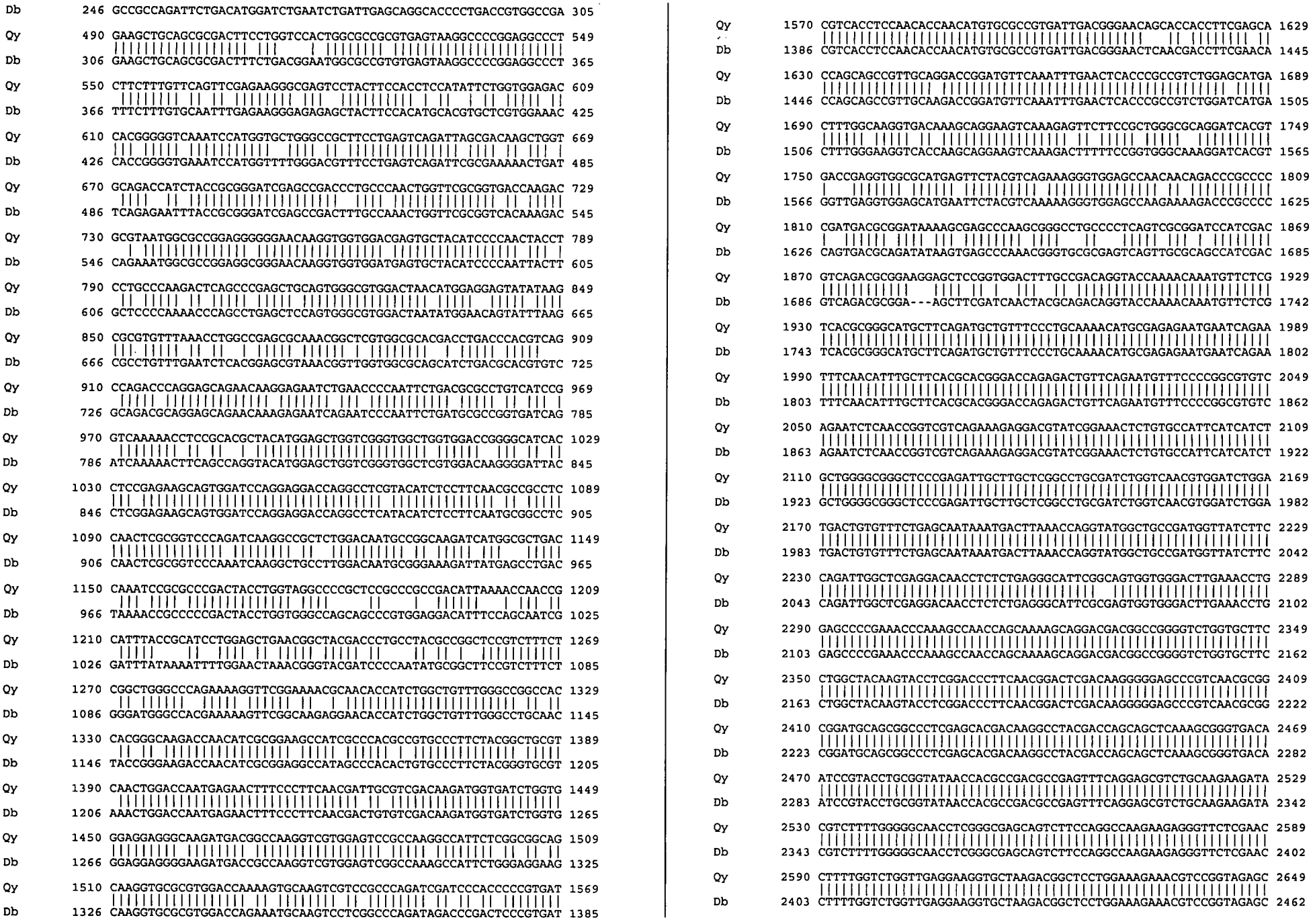

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Qy       2650 AGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGCAGCCCGCTA 2709
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2463 AGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGCAGCCCGCTA 2522

Qy       2710 AAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACCCACAACCTC 2769
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2523 AAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACCCACAACCTC 2582

Qy       2770 TCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGTG 2829
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2583 TCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGTG 2642

Qy       2830 GCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCTCAGGAAATT 2889
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2643 GCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCTCAGGAAATT 2702

Qy       2890 GGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCCGAACATGGG 2949
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Db       2703 GGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCCGAACATGGG 2762

Qy       2950 CCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAACGGGGGCCA 3009
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Db       2763 CCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAACGGGGGCCA 2822

Qy       3010 GCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATTTCAACAGAT 3069
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3070 TCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATTGGGGATTCC 3129
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Db       2883 TCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATTGGGGATTCC 2942

Qy       3130 GGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCACGACGAATG 3189
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Db       2943 GGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCACGACGAATG 3002

Qy       3190 ATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTGTCGGACTCGG 3249
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Db       3003 ATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTCTCGGACTCGG 3062

Qy       3250 AGTACCAGTTCCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTCCGTTCCCGG 3309
             |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3063 AGTACCAGTTGCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTCCGTTCCCGG 3122

Qy       3310 CGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCAGCCAGGCAG 3369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3123 CGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCAGCCAGGCAG 3182

Qy       3370 TGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGAGAACGGGCA 3429
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3183 TGGGACGGTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGAGAACGGGCA 3242

Qy       3430 ATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACGCGCACA 3489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3243 ATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACGCGCACA 3302

Qy       3490 GCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATTACCTGAACA 3549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3303 GCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATTACCTGAACA 3362

Qy       3550 GAACTCACAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCCGTGGGTCTC 3609
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Qy       3610 CAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACCGGCAGCAGC 3669
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Qy       3670 GCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTGGTGCTTCAA 3729
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Db       3483 GCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTGGTGCTTCAA 3542

Qy       3730 AATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGGCCTCACACA 3789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3543 AATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGGCCTCACACA 3602

Qy       3790 AAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAAAGGAGAGCG 3849
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Qy       3850 CCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGGAAATCAAAG 3909
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Qy       3910 CCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCCAGAGCAGCA 3969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3723 CCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCCAGAGCAGCA 3782

Qy       3970 GCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAATGGTGTGGC 4029
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Db       3783 GCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAATGGTGTGGC 3842

Qy       4030 AAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACACGGATGGAC 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3843 AAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACACGGATGGAC 3902

Qy       4090 ACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTCCTCAGATCC 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3903 ACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTCCTCAGATCC 3962

Qy       4150 TCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTACAAAGTTTG 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3963 TCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTACAAAGTTTG 4022

Qy       4210 CTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAATGGGAGCTGC 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4023 CTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAATGGGAGCTGC 4082

Qy       4270 AGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACTATGCAAAAT 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4083 AGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACTATGCAAAAT 4142

Qy       4330 CTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTCGCCCCATTG 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4143 CTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTCGCCCCATTG 4202

Qy       4390 GCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGT 4426
             |||||||||||||||||||||||||||||||||||||
Db       4203 GCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGT 4239
```

RESULT 9
ADZ46598
ID ADZ46598 standard; DNA; 4239 BP.
XX
AC ADZ46598;
XX
DT 30-JUN-2005 (first entry)
XX
DE HSV-AAV sequence rep2cap6 for AAV/HSV vectors.
XX
KW Genetic engineering; gene therapy; vector; cancer; neoplasm; cytostatic;
KW respiratory disease; respiratory-gen.; neurological disease;
KW neuroprotective; ds.
XX
OS Adeno-associated virus.
OS Human herpesvirus 1.
XX
PN WO2005035743-A1.
XX
PD 21-APR-2005.
XX
PF 15-OCT-2003; 2003WO-CN000861.
XX
PR 15-OCT-2003; 2003WO-CN000861.
XX

PA (AGTC-) AGTC GENE TECHNOLOGY CO LTD.
XX
PI Wu X, Cao H, Dong X;
XX
DR WPI; 2005-296279/30.
XX
PT Large-scale production, isolation and purification of serotype adeno-
PT associated virus vectors by infecting cells with recombinant herpes
PT simplex virus vectors, for use in gene therapy of e.g. cancer and
PT respiratory diseases.
XX
PS Claim 1; SEQ ID NO 5; 79pp; Chinese.
XX
CC The invention relates to a recombinant herpes simplex virus (HSV)
CC characterized in that its genome is inserted with a DNA sequence selected
CC from nucleotide sequences of ADZ46594-ADZ46598 or their homologous
CC sequences. Also included are preparing the recombinant HSV (comprising
CC the construction of DNA fragments that contains sequences ADZ46594-
CC ADZ46598, and respectively inserting these 5 DNA fragments into genome of
CC HSV by applying genetic engineering to give the recombinant HSV), large-
CC scale production of 5 serotype recombinant adeno-associated viruses (AAV)
CC 1, 3, 4, 5, and 6 (by preparing the recombinant HSV, establishing a one-
CC strain vector cell i.e. recombinant AAV vector cell-line, infecting the
CC corresponding vector cell-line with the 5 recombinant HSV, producing
CC recombinant AAV under the infective effect of the 5 recombinant HSV in
CC the vector cell-line, separating and purifying the 5 serotype recombinant
CC AAV after lysing the AAV-containing cells and culture liquor to give a
CC crude lysate and further purification of rAAV by density-gradient
CC centrifugation or affinity chromatography) and a recombinant vector
CC plasmid pSNAV-NX (containing ITR at both ends of AAV-1, AAV-3, AAV-4, AAV
CC -5 or AAV-6 genome, with immediate-early enhancer and promoter of
CC cytomegalovirus, and a polyclonal site and a polyA signal, respectively,
CC between the ITR (inverted terminal repeat), and neomycin-resistance gene-
CC expressing cassette at outer edge of ITR). The DNA sequence is inserted
CC into XbaI site in UL2 or UL44 gene in HSV genome. The DNA sequence of
CC sequence ADZ46594-ADZ46598 can also be inserted into other non-essential
CC gene regions in HSV genome. The recombinant HSV is optionally inserted
CC with other DNA sequences homologous with the already-specified fragments.
CC The vectors are for use in gene therapy of e.g. cancer, respiratory
CC diseases and neural diseases. The virus vectors are safe, with long
CC expression time and wide-spectrum of cell infection, even non-cleaved
CC cells and reverse axonal conduction through the incorporated HSV vectors,
CC and high transfer efficiently. The present sequence is the HSV-AAV
CC sequence rep2cap6 for the AAV/HSV vectors of the invention.
XX
SQ Sequence 4239 BP; 1084 A; 1156 C; 1130 G; 869 T; 0 U; 0 Other;

Query Match 81.8%; Score 3831.4; DB 14; Length 4239;
Best Local Similarity 94.3%; Pred. No. 0;
Matches 3997; Conservative 0; Mismatches 236; Indels 4; Gaps 2;

```
Qy      191 GTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCATGTGGTCACGC 250
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Db        6 GTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCATGTGGTCACGC 65

Qy      251 TGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGAGGTTTGAACG 310
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       66 TGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGAGGTTTGAACG 125

Qy      311 CGCAG-CGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGACCTTGACGA 369
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      126 CGCAGCCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGACCTTGACGG 185

Qy      370 GCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGAATGGGAGTT 429
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      186 GCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGAATGGGAGTT 245

Qy      430 GCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGACCGTGGCCGA 489
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      246 GCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGACCGTGGCCGA 305

Qy      490 GAAGCTGCAGCGCGACTTCCTGGTCCACTGGCGCCGCGTGAGTAAGGCCCCGGAGGCCCT 549
            |||||||||||||||||| |||    | ||||||| ||||||||||||||||||||||||

Db      306 GAAGCTGCAGCGCGACTTTCTGACGGAATGGCGCCGTGTGAGTAAGGCCCCGGAGGCCCT 365

Qy      550 CTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTACTTCCACCTCCATATTCTGGTGGAGAC 609
            |||||||| || || |||||||| ||| |||||||||| | ||  | || ||||| ||
Db      366 TTTCTTTGTGCAATTTGAGAAGGGAGAGAGCTACTTCCACATGCACGTGCTCGTGGAAAC 425

Qy      610 CACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGCGACAAGCTGGT 669
            ||| ||||| |||||||||||  |||| || ||||||||||||||| |||| || ||| |
Db      426 CACCGGGGTGAAATCCATGGTTTTGGGACGTTTCCTGAGTCAGATTCGCGAAAAACTGAT 485

Qy      670 GCAGACCATCTACCGCGGGATCGAGCCGACCCTGCCCAACTGGTTCGCGGTGACCAAGAC 729
            ||||  || ||||||||||||||||||||  |||| |||||||||||||| || |||||
Db      486 TCAGAGAATTTACCGCGGGATCGAGCCGACTTTGCCAAACTGGTTCGCGGTCACAAAGAC 545

Qy      730 GCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCCCCAACTACCT 789
            | |||||||||||||| |||||||||||||||||| |||||||||||||||||| ||| |
Db      546 CAGAAATGGCGCCGGAGGCGGGAACAAGGTGGTGGATGAGTGCTACATCCCCAATTACTT 605

Qy      790 CCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGGAGTATATAAG 849
            || ||||| || ||||| ||||| |||||||||||||||||| |||||  ||||| ||||
Db      606 GCTCCCCAAAACCCAGCCTGAGCTCCAGTGGGCGTGGACTAATATGGAACAGTATTTAAG 665

Qy      850 CGCGTGTTTAAACCTGGCCGAGCGCAAACGGCTCGTGGCGCACGACCTGACCCACGTCAG 909
            ||| ||||| || ||  | ||||| |||||| | |||||||  | ||||| |||||
Db      666 CGCCTGTTTGAATCTCACGGAGCGTAAACGGTTGGTGGCGCAGCATCTGACGCACGTGTC 725

Qy      910 CCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGCCTGTCATCCG 969
            ||||| |||||||||||||| ||||||| ||| |||||||||| ||||| || ||| |
Db      726 GCAGACGCAGGAGCAGAACAAAGAGAATCAGAATCCCAATTCTGATGCGCCGGTGATCAG 785

Qy      970 GTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACCGGGGCATCAC 1029
            |||||||| || ||  | |||||||||||||||||||||| ||||||  ||| || ||
Db      786 ATCAAAAACTTCAGCCAGGTACATGGAGCTGGTCGGGTGGCTCGTGGACAAGGGGATTAC 845

Qy      1030 CTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCAACGCCGCCTC 1089
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Qy      1090 CAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCATGGCGCTGAC 1149
             |||||||||||||| |||||||| ||  |||||||||| || ||||| |||   |||||
Db       906 CAACTCGCGGTCCCAAATCAAGGCTGCCTTGGACAATGCGGGAAAGATTATGAGCCTGAC 965

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             ||| |||| |||||||||||||| ||||      ||     |  |||||   | ||| ||
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Qy      1270 CGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTTTGGGCCGGCCAC 1329
             || ||||||  ||||| |||||| ||  | |||||||||||||||||||||| || ||
Db      1086 GGGATGGGCCACGAAAAAGTTCGGCAAGAGGAACACCATCTGGCTGTTTGGGCCTGCAAC 1145

Qy      1330 CACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCTACGGCTGCGT 1389
             || || |||||||||||||| ||||| ||||||  | |||||||||||||| |||||
Db      1146 TACCGGGAAGACCAACATCGCGGAGGCCATAGCCCACACTGTGCCCTTCTACGGGTGCGT 1205

Qy      1390 CAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGGTGATCTGGTG 1449
             |||||||||||||||||||||||||||||| || ||||||||||||||||||||||||
Db      1206 AAACTGGACCAATGAGAACTTTCCCTTCAACGACTGTGTCGACAAGATGGTGATCTGGTG 1265

Qy      1450 GGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTCTCGGCGGCAG 1509
             ||||||||| |||||||| |||||||||||||||| ||||| |||||||| || || ||
Db      1266 GGAGGAGGGGAAGATGACCGCCAAGGTCGTGGAGTCGGCCAAAGCCATTCTGGGAGGAAG 1325

Qy      1510 CAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTCCGCCCAGATCGATCCCACCCCCGTGAT 1569
             |||||||||||||||||| || |||||||| || |||||||| || || || ||||||||
Db      1326 CAAGGTGCGCGTGGACCAGAAATGCAAGTCCTCGGCCCAGATAGACCCGACTCCCGTGAT 1385

Qy      1570 CGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACAGCACCACCTTCGAGCA 1629
             |||||||||||||||||||||||||||||||||||||||||||||   || |||||||| ||
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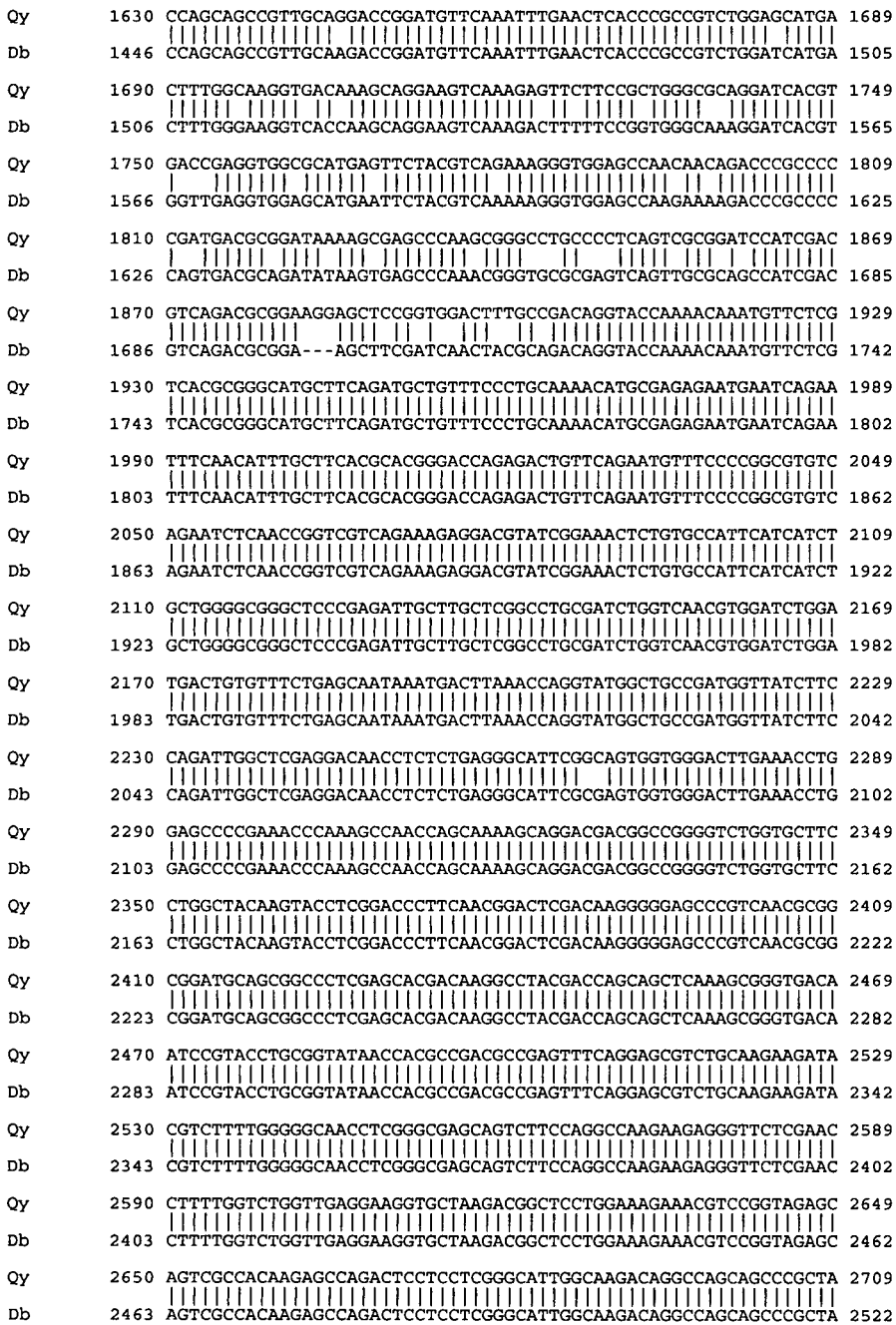
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Db 1506 CTTTGGGAAGGTCACCAAGCAGGAAGTCAAAGACTTTTTCCGGTGGGCAAAGGATCACGT 1565
Qy 1750 GACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAACAGACCCGCCCC 1809
Db 1566 GGTTGAGGTGGAGCATGAATTCTACGTCAAAAAGGGTGGAGCCAAGAAAAGACCCGCCCC 1625
Qy 1810 CGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGATCCATCGAC 1869
Db 1626 CAGTGACGCAGATATAAGTGAGCCCAAACGGGTGCGCGAGTCAGTTGCGCAGCCATCGAC 1685
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Db 1686 GTCAGACGCGGA---AGCTTCGATCAACTACGCAGACAGGTACCAAAACAAATGTTCTCG 1742
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Db 1743 TCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGAATGAATCAGAA 1802
Qy 1990 TTTCAACATTTGCTTCACGCACGGGACCAGAGACTGTTCAGAATGTTTCCCCGGCGTGTC 2049
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Db 1863 AGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCATTCATCATCT 1922
Qy 2110 GCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGTGGATCTGGA 2169
Db 1923 GCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGTGGATCTGGA 1982
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Qy 2230 CAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGGCAGTGGTGGGACTTGAAACCTG 2289
Db 2043 CAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGGACTTGAAACCTG 2102
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Db 2103 GAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTCTGGTGCTTC 2162
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Db 2163 CTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCGTCAACGCGG 2222
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Db 2223 CGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAGCGGGTGACA 2282
Qy 2470 ATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATA 2529
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Db 2343 CGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGAGGGTTCTCGAAC 2402
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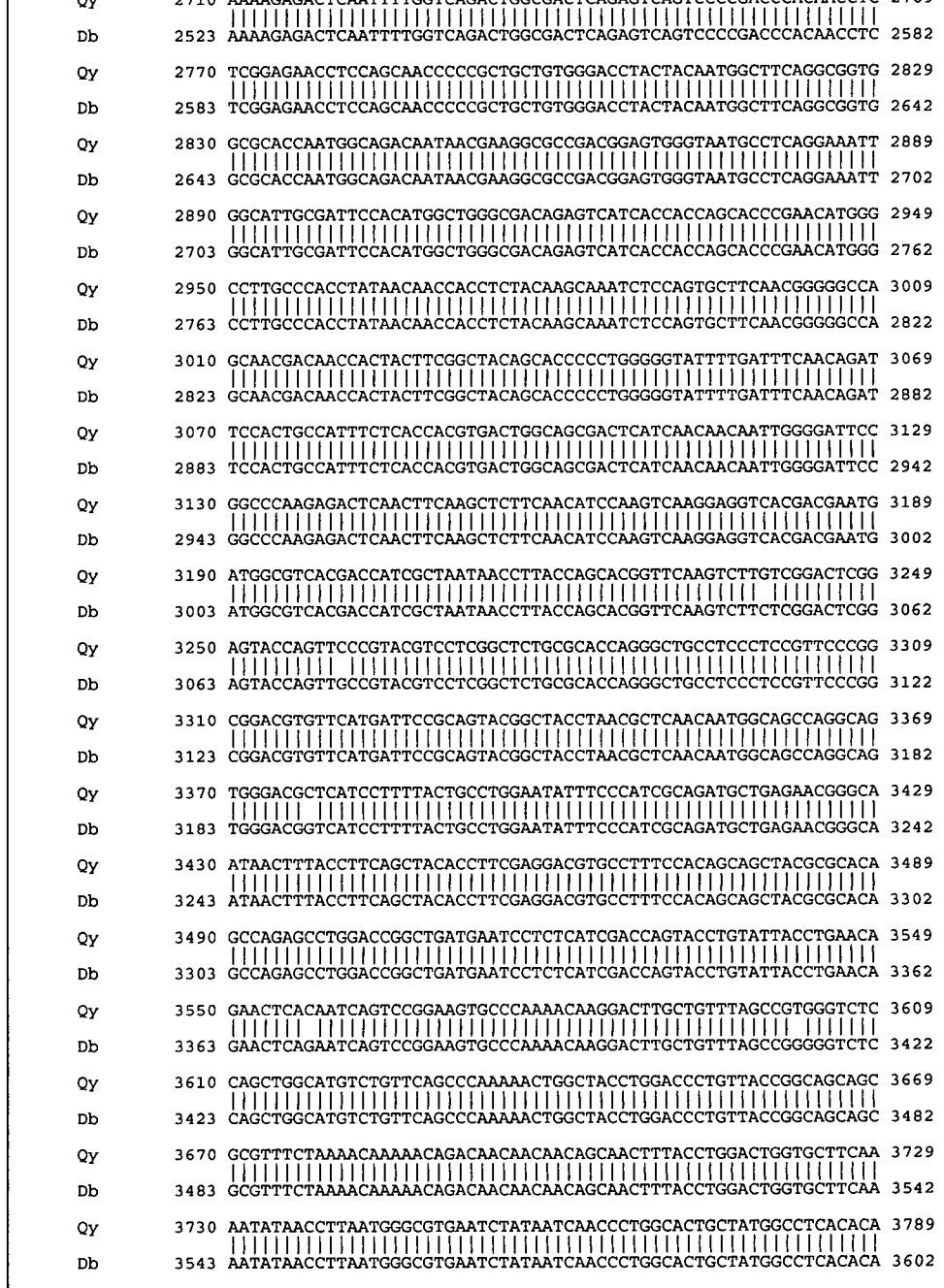
Db 2403 CTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCCTGGAAAGAAACGTCCGGTAGAGC 2462
Qy 2650 AGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGCAGCCCGCTA 2709
Db 2463 AGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGCAGCCCGCTA 2522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Db 2523 AAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACCCACAACCTC 2582
Qy 2770 TCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGTG 2829
Db 2583 TCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGTG 2642
Qy 2830 GCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCTCAGGAAATT 2889
Db 2643 GCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCTCAGGAAATT 2702
Qy 2890 GGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCCGAACATGGG 2949
Db 2703 GGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCCGAACATGGG 2762
Qy 2950 CCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAACGGGGGCCA 3009
Db 2763 CCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAACGGGGGCCA 2822
Qy 3010 GCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATTTCAACAGAT 3069
Db 2823 GCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATTTCAACAGAT 2882
Qy 3070 TCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATTGGGGATTCC 3129
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Db 3003 ATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTCTCGGACTCGG 3062
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Qy 3370 TGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGAGAACGGGCA 3429
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Qy 3550 GAACTCACAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCCGTGGGTCTC 3609
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Qy 3790 AAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAAAGGAGAGCG 3849

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Qy       3850 CCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGGAAATCAAAG 3909
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Qy       3910 CCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCCAGAGCAGCA 3969
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Qy       4030 AAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACACGGATGGAC 4089
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Qy       4090 ACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTCCTCAGATCC 4149
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Qy       4150 TCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTACAAAGTTTG 4209
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Qy       4210 CTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAATGGGAGCTGC 4269
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Qy       4270 AGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACTATGCAAAAT 4329
Db       4083 AGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACTATGCAAAAT 4142

Qy       4330 CTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTCGCCCCATTG 4389
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Qy       4390 GCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGT 4426
Db       4203 GCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGT 4239
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RESULT 10
ADW39398
ID ADW39398 standard; DNA; 4347 BP.
XX
AC ADW39398;
XX
DT 24-MAR-2005 (first entry)
XX
DE Adeno-associated virus 2 (AAV2) rep-AAV1 cap fusion DNA - SEQ ID 1.
XX
KW genetically engineered microorganism; vector; rep; cap; ds.
XX
OS Adeno-associated virus 2.
OS Chimeric.
OS Unidentified.
XX
PN CN1461805-A.
XX
PD 17-DEC-2003.
XX
PF 27-MAY-2002; 2002CN-00117965.
XX
PR 27-MAY-2002; 2002CN-00117965.
XX
PA (BENY-) BENYUAN ZHENGYANG GENETIC TECHNOLOGY CO.
XX
PI Wu X, Cao H, Dong X;
XX
DR WPI; 2004-248658/24.
XX
PT Structure of a recombinant herpes simplex virus and its use.
XX
PS Claim 1; SEQ ID NO 1; 102pp; Chinese.
XX
CC The invention relates to a novel recombinant herpes simplex virus (rHSVS)
CC whose genome is respectively inserted by the Adeno-associated virus (AAV)
CC rep gene and cap gene. The AVV genes may be derived from viruses AAV1,
CC AAV2, AAV3, AAV4, AAV5 and AAV6. The methods of the invention may be
CC useful for generating recombinant vectors with high efficiency and no
CC need of reconfiguration. The current sequence is that of the Adeno-
CC associated virus 2 (AAV2) rep-Adeno-associated virus 1 (AAV1) cap fusion
CC DNA (SEQ ID 1) of the invention.
XX
SQ Sequence 4347 BP; 1106 A; 1186 C; 1142 G; 913 T; 0 U; 0 Other;

```
  Query Match            81.2%;  Score 3802;  DB 13;  Length 4347;
  Best Local Similarity  92.6%;  Pred. No. 0;
  Matches 4026;  Conservative    0;  Mismatches  315;  Indels    5;  Gaps    3;

Qy        191 GTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCATGTGGTCACGC 250
Db          6 GTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCATGTGGTCACGC 65

Qy        251 TGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGAGGTTTGAACG 310
Db         66 TGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGAGGTTTGAACG 125

Qy        311 CGCAG-CGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGACCTTGACGA 369
Db        126 CGCAGCCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGACCTTGACGG 185

Qy        370 GCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGAATGGGAGTT 429
Db        186 GCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGAATGGGAGTT 245

Qy        430 GCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGACCGTGGCCGA 489
Db        246 GCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGACCGTGGCCGA 305

Qy        490 GAAGCTGCAGCGCGACTTCCTGGTCCACTGGCGCCGCGTGAGTAAGGCCCCGGAGGCCCT 549
Db        306 GAAGCTGCAGCGCGACTTTCTGACGGAATGGCGCCGTGTGAGTAAGGCCCCGGAGGCCCT 365

Qy        550 CTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTACTTCCACCTCCATATTCTGGTGGAGAC 609
Db        366 TTTCTTTGTGCAATTTGAGAAGGGAGAGAGCTACTTCCACATGCACGTGCTCGTGGAAAC 425

Qy        610 CACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGCGACAAGCTGGT 669
Db        426 CACCGGGGTGAAATCCATGGTTTTGGGACGTTTCCTGAGTCAGATTCGCGAAAAACTGAT 485

Qy        670 GCAGACCATCTACCGCGGGATCGAGCCGACCCTGCCCAACTGGTTCGCGGTGACCAAGAC 729
Db        486 TCAGAGAATTTACCGCGGGATCGAGCCGACTTTGCCAAACTGGTTCGCGGTCACAAAGAC 545

Qy        730 GCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCCCCAACTACCT 789
Db        546 CAGAAATGGCGCCGGAGGCGGGAACAAGGTGGTGGATGAGTGCTACATCCCCAATTACTT 605

Qy        790 CCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGGAGTATATAAG 849
Db        606 GCTCCCCAAAACCCAGCCTGAGCTCCAGTGGGCGTGGACTAATATGGAACAGTATTTAAG 665

Qy        850 CGCGTGTTTAAACCTGGCCGAGCGCAAACGGCTCGTGGCGCACGACCTGACCCACGTCAG 909
Db        666 CGCCTGTTTGAATCTCACGGAGCGTAAACGGTTGGTGGCGCAGCATCTGACGCACGTGTC 725

Qy        910 CCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGCCTGTCATCCG 969
Db        726 GCAGACGCAGGAGCAGAACAAAGAGAATCAGAATCCCAATTCTGATGCGCCGGTGATCAG 785

Qy        970 GTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACCGGGGCATCAC 1029
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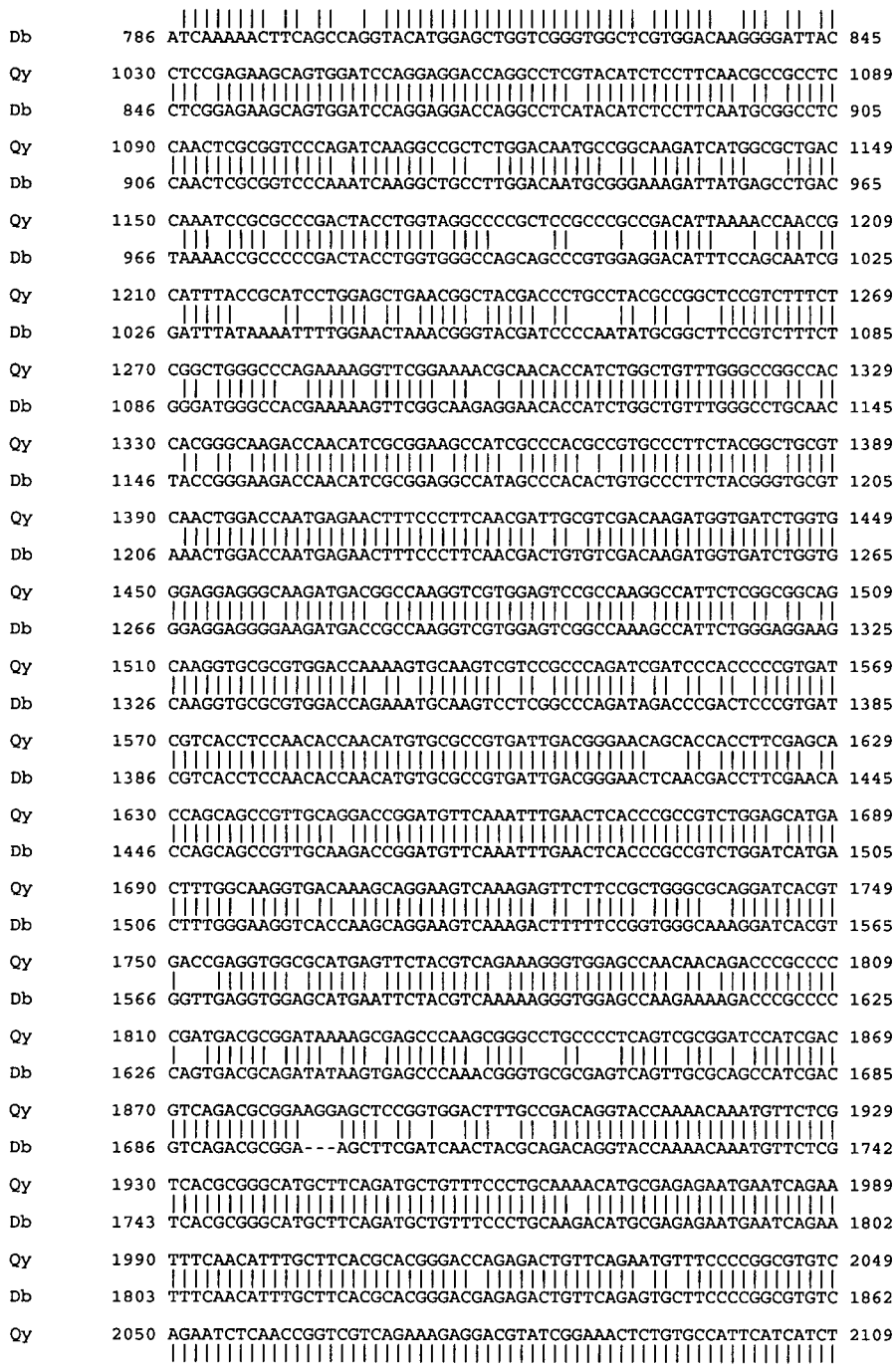
Db 786 ATCAAAAACTTCAGCCAGGTACATGGAGCTGGTCGGGTGGCTCGTGGACAAGGGGATTAC 845
Qy 1030 CTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCAACGCCGCCTC 1089
Db 846 CTCGGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCATACATCTCCTTCAATGCGGCCTC 905
Qy 1090 CAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCATGGCGCTGAC 1149
Db 906 CAACTCGCGGTCCCAAATCAAGGCTGCCTTGGACAATGCGGGAAAGATTATGAGCCTGAC 965
Qy 1150 CAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACATTAAAACCAACCG 1209
Db 966 TAAAACCGCCCCCGACTACCTGGTGGGCCAGCAGCCCGTGGAGGACATTTCCAGCAATCG 1025
Qy 1210 CATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCTCCGTCTTTCT 1269
Db 1026 GATTTATAAAATTTTGGAACTAAACGGGTACGATCCCCAATATGCGGCTTCCGTCTTTCT 1085
Qy 1270 CGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTTTGGGCCGGCCAC 1329
Db 1086 GGGATGGGCCACGAAAAAGTTCGGCAAGAGGAACACCATCTGGCTGTTTGGGCCTGCAAC 1145
Qy 1330 CACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCTACGGCTGCGT 1389
Db 1146 TACCGGGAAGACCAACATCGCGGAGGCCATAGCCCACACTGTGCCCTTCTACGGGTGCGT 1205
Qy 1390 CAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGGTGATCTGGTG 1449
Db 1206 AAACTGGACCAATGAGAACTTTCCCTTCAACGACTGTGTCGACAAGATGGTGATCTGGTG 1265
Qy 1450 GGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTCTCGGCGGCAG 1509
Db 1266 GGAGGAGGGGAAGATGACCGCCAAGGTCGTGGAGTCGGCCAAAGCCATTCTGGGAGGAAG 1325
Qy 1510 CAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTCCGCCCAGATCGATCCCACCCCCGTGAT 1569
Db 1326 CAAGGTGCGCGTGGACCAGAAATGCAAGTCCTCGGCCCAGATAGACCCGACTCCCGTGAT 1385
Qy 1570 CGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACAGCACCACCTTCGAGCA 1629
Db 1386 CGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACTCAACGACCTTCGAACA 1445
Qy 1630 CCAGCAGCCGTTGCAGGACCGGATGTTCAAATTTGAACTCACCCGCCGTCTGGAGCATGA 1689
Db 1446 CCAGCAGCCGTTGCAAGACCGGATGTTCAAATTTGAACTCACCCGCCGTCTGGATCATGA 1505
Qy 1690 CTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGAGTTCTTCCGCTGGGCGCAGGATCACGT 1749
Db 1506 CTTTGGGAAGGTCACCAAGCAGGAAGTCAAAGACTTTTTCCGGTGGGCAAAGGATCACGT 1565
Qy 1750 GACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAACAGACCCGCCCC 1809
Db 1566 GGTTGAGGTGGAGCATGAATTCTACGTCAAAAAGGGTGGAGCCAAGAAAAGACCCGCCCC 1625
Qy 1810 CGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGATCCATCGAC 1869
Db 1626 CAGTGACGCAGATATAAGTGAGCCCAAACGGGTGCGCGAGTCAGTTGCGCAGCCATCGAC 1685
Qy 1870 GTCAGACGCGGAAGGAGCTCCGGTGGACTTTGCCGACAGGTACCAAAACAAATGTTCTCG 1929
Db 1686 GTCAGACGCGGA---AGCTTCGATCAACTACGCAGACAGGTACCAAAACAAATGTTCTCG 1742
Qy 1930 TCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGAATGAATCAGAA 1989
Db 1743 TCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAGACATGCGAGAGAATGAATCAGAA 1802
Qy 1990 TTTCAACATTTGCTTCACGCACGGGACCAGAGACTGTTCAGAATGTTTCCCCGGCGTGTC 2049
Db 1803 TTTCAACATTTGCTTCACGCACGGGACGAGAGACTGTTCAGAGTGCTTCCCCGGCGTGTC 1862
Qy 2050 AGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCATTCATCATCT 2109
Db 1863 AGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCATTCATCATCT 1922
Qy 2110 GCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGTGGATCTGGA 2169
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Qy 2230 CAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGGCAGTGGTGGGACTTGAAACCTG 2289
Db 2043 CAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGGACTTGAAACCTG 2102
Qy 2290 GAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTCTGGTGCTTC 2349
Db 2103 GAGCCCCGAAGCCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTCTGGTGCTTC 2162
Qy 2350 CTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCGTCAACGCGG 2409
Db 2163 CTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCGTCAACGCGG 2222
Qy 2410 CGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAGCGGGTGACA 2469
Db 2223 CGGACGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAGCGGGTGACA 2282
Qy 2470 ATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATA 2529
Db 2283 ATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATA 2342
Qy 2530 CGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGAGGGTTCTCGAAC 2589
Db 2343 CGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGCGGGTTCTCGAAC 2402
Qy 2590 CTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCCTGGAAAGAAACGTCCGGTAGAGC 2649
Db 2403 CTCTCGGTCTGGTTGAGGAAGGCGCTAAGACGGCTCCTGGAAAGAAACGTCCGGTAGAGC 2462
Qy 2650 AGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGCAGCCCGCTA 2709
Db 2463 AGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATCGGCAAGACAGGCCAGCAGCCCGCTA 2522
Qy 2710 AAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACCCACAACCTC 2769
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Qy 2770 TCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGTG 2829
Db 2583 TCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGTG 2642
Qy 2830 GCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCTCAGGAAATT 2889
Db 2643 GCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCTCAGGAAATT 2702
Qy 2890 GGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCCGAACATGGG 2949
Db 2703 GGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCCGCACCTGGG 2762
Qy 2950 CCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAACGGGGGCCA 3009
Db 2763 CCTTGCCCACCTACAATAACCACCTCTACAAGCAAATCTCCAGTGCTTCAACGGGGGCCA 2822
Qy 3010 GCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATTTCAACAGAT 3069
Db 2823 GCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATTTCAACAGAT 2882
Qy 3070 TCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATTGGGGATTCC 3129
Db 2883 TCCACTGCCACTTTTCACCACGTGACTGGCAGCGACTCATCAACAACAATTGGGGATTCC 2942
Qy 3130 GGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCACGACGAATG 3189
Db 2943 GGCCCAAGAGACTCAACTTCAAACTCTTCAACATCCAAGTCAAGGAGGTCACGACGAATG 3002

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Qy       3190 ATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTGTCGGACTCGG 3249
             |||||||||| |||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       3003 ATGGCGTCACAACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTCTCGGACTCGG 3062

Qy       3250 AGTACCAGTTCCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTCCGTTCCCGG 3309
             |||||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3063 AGTACCAGCTTCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTCCGTTCCCGG 3122

Qy       3310 CGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCAGCCAGGCAG 3369
             |||||||||||||||||||||||| |||||||||| |||||||||||||||||||| || |
Db       3123 CGGACGTGTTCATGATTCCGCAATACGGCTACCTGACGCTCAACAATGGCAGCCAAGCCG 3182

Qy       3370 TGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGAGAACGGGCA 3429
             ||||||| |||||||||||||||||||||||||| || ||||||||||||||||||||
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Qy       3430 ATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACGCGCACA 3489
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Qy       3490 GCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATTACCTGAACA 3549
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
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Qy       3550 GAACTCACAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCCGTGGGTCTC 3609
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3363 GAACTCAAAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCCGTGGGTCTC 3422

Qy       3610 CAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACCGGCAGCAGC 3669
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
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Qy       3670 GCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTGGTGCTTCAA 3729
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Db       3483 GCGTTTCTAAAACAAAAACAGACAACAACAACAGCAATTTTACCTGGACTGGTGCTTCAA 3542

Qy       3730 AATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGGCCTCACACA 3789
             |||||||||| |||||||||||||| || ||||||||||||||||||||||||||||||||
Db       3543 AATATAACCTCAATGGGCGTGAATCCATCATCAACCCTGGCACTGCTATGGCCTCACACA 3602

Qy       3790 AAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAAAGGAGAGCG 3849
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Qy       3850 CCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGGAAATCAAAG 3909
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Db       3723 CCACTAACCCTGTGGCCACCGAAAGATTTGGGACCGTGGCAGTCAATTTCCAGAGCAGCA 3782

Qy       3970 GCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAATGGTGTGGC 4029
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Qy       4030 AAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACACGGATGGAC 4089
             |||| |||||||| |||||||||||||||| |||||||||||||||||||||||| |||||||
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Qy       4090 ACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTCCTCAGATCC 4149
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Qy       4150 TCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTACAAAGTTTG 4209
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Qy       4210 CTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAATGGGAGCTGC 4269
             |||||||||||||| || |||||||||||||||| ||||| ||||||||||||||||||||
Db       4023 CTTCATTCATCACCCAATACTCCACAGGACAAGTGAGTGTGGAAATTGAATGGGAGCTGC 4082

Qy       4270 AGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACTATGCAAAAT 4329
             |||||||||||||||| |||||||||||||||||||||||| ||||| || ||||||||||
Db       4083 AGAAAGAAAACAGCAAGCGCTGGAATCCCGAAGTGCAGTACACATCCAATTATGCAAAAT 4142

Qy       4330 CTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTCGCCCCATTG 4389
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       4143 CTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTATACTGAGCCTCGCCCCATTG 4202

Qy       4390 GCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCGGTTAATTCG 4449
             |||||||||||||| |||||||||||||||||  |||||||||||||||||||| |||||
Db       4203 GCACCCGTTACCTTACCCGTCCCCTGTAATTACGTGTTAATCAATAAACCGGTTGATTCG 4262

Qy       4450 TGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCACCATAGCAACCGGT 4509
             | |||||||||||||||||||| ||||||| |||||||||| ||| ||||| |  |  | |
Db       4263 TTTCAGTTGAACTTTGGTCTCCTGTCCTTCTTATCTTATC-GGTTACCATGGTTATAGCT 4321

Qy       4510 TACACATTAACTGCTTAGTTGCGCTT 4535
             ||||||||||||||| |||||||||
Db       4322 TACACATTAACTGCTTGGTTGCGCTT 4347
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RESULT 11
ADZ46594
ID ADZ46594 standard; DNA; 4347 BP.
XX
AC ADZ46594;
XX
DT 30-JUN-2005 (first entry)
XX
DE HSV-AAV sequence rep2cap1 for AAV/HSV vectors.
XX
KW Genetic engineering; gene therapy; vector; cancer; neoplasm; cytostatic;
KW respiratory disease; respiratory-gen.; neurological disease;
KW neuroprotective; ds.
XX
OS Adeno-associated virus.
OS Human herpesvirus 1.
XX
PN WO2005035743-A1.
XX
PD 21-APR-2005.
XX
PF 15-OCT-2003; 2003WO-CN000861.
XX
PR 15-OCT-2003; 2003WO-CN000861.
XX
PA (AGTC-) AGTC GENE TECHNOLOGY CO LTD.
XX
PI Wu X, Cao H, Dong X;
XX
DR WPI; 2005-296279/30.
XX
PT Large-scale production, isolation and purification of serotype adeno-
PT associated virus vectors by infecting cells with recombinant herpes
PT simplex virus vectors, for use in gene therapy of e.g. cancer and
PT respiratory diseases.
XX
PS Claim 1; SEQ ID NO 1; 79pp; Chinese.
XX
CC The invention relates to a recombinant herpes simplex virus (HSV)
CC characterized in that its genome is inserted with a DNA sequence selected
CC from nucleotide sequences of ADZ46594-ADZ46598 or their homologous
CC sequences. Also included are preparing the recombinant HSV (comprising
CC the construction of DNA fragments that contains sequences ADZ46594-
CC ADZ46598, and respectively inserting these 5 DNA fragments into genome of
CC HSV by applying genetic engineering to give the recombinant HSV), large-
CC scale production of 5 serotype recombinant adeno-associated viruses (AAV)
CC 1, 3, 4, 5, and 6 (by preparing the recombinant HSV, establishing a one-
CC strain vector cell i.e. recombinant AAV vector cell-line, infecting the
CC corresponding vector cell-line with the 5 recombinant HSV, producing
CC recombinant AAV under the infective effect of the 5 recombinant HSV in
CC the vector cell-line, separating and purifying the 5 serotype recombinant
CC AAV after lysing the AAV-containing cells and culture liquor to give a

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CC   crude lysate and further purification of rAAV by density-gradient
CC   centrifugation or affinity chromatography) and a recombinant vector
CC   plasmid pSNAV-NX (containing ITR at both ends of AAV-1, AAV-3, AAV-4, AAV
CC   -5 or AAV-6 genome, with immediate-early enhancer and promoter of
CC   cytomegalovirus, and a polyclonal site and a polyA signal, respectively,
CC   between the ITR (inverted terminal repeat), and neomycin-resistance gene-
CC   expressing cassette at outer edge of ITR). The DNA sequence is inserted
CC   into XbaI site in UL2 or UL44 gene in HSV genome. The DNA sequence of
CC   sequence ADZ46594-ADZ46598 can also be inserted into other non-essential
CC   gene regions in HSV genome. The recombinant HSV is optionally inserted
CC   with other DNA sequences homologous with the already-specified fragments.
CC   The vectors are for use in gene therapy of e.g. cancer, respiratory
CC   diseases and neural diseases. The virus vectors are safe, with long
CC   expression time and wide-spectrum of cell infection, even non-cleaved
CC   cells and reverse axonal conduction through the incorporated HSV vectors,
CC   and high transfer efficiently. The present sequence is the HSV-AAV
CC   sequence rep2cap1 for the AAV/HSV vectors of the invention.
XX
SQ   Sequence 4347 BP; 1106 A; 1186 C; 1142 G; 913 T; 0 U; 0 Other;

  Query Match             81.2%;  Score 3802;  DB 14;  Length 4347;
  Best Local Similarity   92.6%;  Pred. No. 0;
  Matches 4026;  Conservative    0;  Mismatches  315;  Indels    5;  Gaps    3;

Qy        191 GTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCATGTGGTCACGC 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCATGTGGTCACGC 65

Qy        251 TGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGAGGTTTGAACG 310
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Db         66 TGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGAGGTTTGAACG 125

Qy        311 CGCAG-CGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGACCTTGACGA 369
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CGCAGCCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGACCTTGACGG 185

Qy        370 GCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGAATGGGAGTT 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGAATGGGAGTT 245

Qy        430 GCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGACCGTGGCCGA 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGACCGTGGCCGA 305

Qy        490 GAAGCTGCAGCGCGACTTCCTGGTCCACTGGCGCCGCGTGAGTAAGGCCCCGGAGGCCCT 549
              |||||||||||||||||| |||    | ||||||| ||||||||||||||||||||||||
Db        306 GAAGCTGCAGCGCGACTTTCTGACGGAATGGCGCCGTGTGAGTAAGGCCCCGGAGGCCCT 365

Qy        550 CTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTACTTCCACCTCCATATTCTGGTGGAGAC 609
              |||||||| || || |||||||| |||  |||||||||| | ||  | || ||||| ||
Db        366 TTTCTTTGTGCAATTTGAGAAGGGAGAGAGCTACTTCCACATGCACGTGCTCGTGGAAAC 425

Qy        610 CACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGCGACAAGCTGGT 669
              ||| ||||| |||||||||||  |||| || ||||||||||||||| |||| || ||| |
Db        426 CACCGGGGTGAAATCCATGGTTTTGGGACGTTTCCTGAGTCAGATTCGCGAAAAACTGAT 485

Qy        670 GCAGACCATCTACCGCGGGATCGAGCCGACCCTGCCCAACTGGTTCGCGGTGACCAAGAC 729
              ||||  || ||||||||||||||||||  |||| |||||||||||| || |||||
Db        486 TCAGAGAATTTACCGCGGGATCGAGCCGACTTTGCCAAACTGGTTCGCGGTCACAAAGAC 545

Qy        730 GCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCCCCAACTACCT 789
              | |||||||||||||| ||||||||||||||||| |||||||||||||||||| ||| |
Db        546 CAGAAATGGCGCCGGAGGCGGGAACAAGGTGGTGGATGAGTGCTACATCCCCAATTACTT 605

Qy        790 CCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGGAGTATATAAG 849
              || ||||| || ||||| ||||| |||||||||||||||| |||||  ||||| ||||
Db        606 GCTCCCCAAAACCCAGCCTGAGCTCCAGTGGGCGTGGACTAATATGGAACAGTATTTAAG 665

Qy        850 CGCGTGTTTAAACCTGGCCGAGCGCAAACGGCTCGTGGCGCACGACCTGACCCACGTCAG 909
              ||| ||||| || ||  | ||||| |||||| | ||||||||  | |||||  |||||
Db        666 CGCCTGTTTGAATCTCACGGAGCGTAAACGGTTGGTGGCGCAGCATCTGACGCACGTGTC 725

Qy        910 CCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGCCTGTCATCCG 969
              |||||| |||||||||||||| ||||||| ||| |||||||||| ||||| || ||| |
Db        726 GCAGACGCAGGAGCAGAACAAAGAGAATCAGAATCCCAATTCTGATGCGCCGGTGATCAG 785

Qy        970 GTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACCGGGGCATCAC 1029
              |||||||| || ||  | |||||||||||||||||||||||||| ||||||  ||| || ||
Db        786 ATCAAAAACTTCAGCCAGGTACATGGAGCTGGTCGGGTGGCTCGTGGACAAGGGGATTAC 845

Qy       1030 CTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCAACGCCGCCTC 1089
              ||| |||||||||||||||||||||||||||||| |||||||||||||| || |||||
Db        846 CTCGGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCATACATCTCCTTCAATGCGGCCTC 905

Qy       1090 CAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCATGGCGCTGAC 1149
              |||||||||||||| |||||||| ||  ||||||||| || ||||| |||   |||||
Db        906 CAACTCGCGGTCCCAAATCAAGGCTGCCTTGGACAATGCGGGAAAGATTATGAGCCTGAC 965

Qy       1150 CAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACATTAAAACCAACCG 1209
              ||| |||| |||||||||||||| ||||      ||     | ||||||   | ||| ||
Db        966 TAAAACCGCCCCCGACTACCTGGTGGGCCAGCAGCCCGTGGAGGACATTTCCAGCAATCG 1025

Qy       1210 CATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCTCCGTCTTTCT 1269
              |||||    ||  |||| || ||||| ||||| ||     || || | ||||||||||
Db       1026 GATTTATAAAATTTTGGAACTAAACGGGTACGATCCCCAATATGCGGCTTCCGTCTTTCT 1085

Qy       1270 CGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTTTGGGCCGGCCAC 1329
              || ||||||  ||||| |||||| ||  | |||||||||||||||||||| || ||
Db       1086 GGGATGGGCCACGAAAAAGTTCGGCAAGAGGAACACCATCTGGCTGTTTGGGCCTGCAAC 1145

Qy       1330 CACGGGCAAGACCAACATCGCGGAAGCCATCGCCCACGCCGTGCCCTTCTACGGCTGCGT 1389
              || || |||||||||||||||| ||||| |||||| | |||||||||||||| |||||
Db       1146 TACCGGGAAGACCAACATCGCGGAGGCCATAGCCCACACTGTGCCCTTCTACGGGTGCGT 1205

Qy       1390 CAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGGTGATCTGGTG 1449
              |||||||||||||||||||||||||||||||| || ||||||||||||||||||||||
Db       1206 AAACTGGACCAATGAGAACTTTCCCTTCAACGACTGTGTCGACAAGATGGTGATCTGGTG 1265

Qy       1450 GGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTCTCGGCGGCAG 1509
              ||||||||| |||||||| |||||||||||||||| ||||| |||||||| || || ||
Db       1266 GGAGGAGGGGAAGATGACCGCCAAGGTCGTGGAGTCGGCCAAAGCCATTCTGGGAGGAAG 1325

Qy       1510 CAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTCCGCCCAGATCGATCCCACCCCCGTGAT 1569
              |||||||||||||||||| || |||||||| || |||||||| || || || ||||||||
Db       1326 CAAGGTGCGCGTGGACCAGAAATGCAAGTCCTCGGCCCAGATAGACCCGACTCCCGTGAT 1385

Qy       1570 CGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACAGCACCACCTTCGAGCA 1629
              |||||||||||||||||||||||||||||||||||||||||||||    || |||||||| ||
Db       1386 CGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACTCAACGACCTTCGAACA 1445

Qy       1630 CCAGCAGCCGTTGCAGGACCGGATGTTCAAATTTGAACTCACCCGCCGTCTGGAGCATGA 1689
              |||||||||||||| |||||||||||||||||||||||||||||||||||||||| |||||
Db       1446 CCAGCAGCCGTTGCAAGACCGGATGTTCAAATTTGAACTCACCCGCCGTCTGGATCATGA 1505

Qy       1690 CTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGAGTTCTTCCGCTGGGCGCAGGATCACGT 1749
              |||||| ||||| || |||||||||||||||| || ||||| |||||  ||||||||||
Db       1506 CTTTGGGAAGGTCACCAAGCAGGAAGTCAAAGACTTTTTCCGGTGGGCAAAGGATCACGT 1565

Qy       1750 GACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAACAGACCCGCCCC 1809
              |   ||||||| |||||| |||||||||| |||||||||||||||| || ||||||||||
Db       1566 GGTTGAGGTGGAGCATGAATTCTACGTCAAAAAGGGTGGAGCCAAGAAAAGACCCGCCCC 1625

Qy       1810 CGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGATCCATCGAC 1869
              |  |||||| |||| ||| |||||||| ||||    ||    |||| ||| | ||||||||
Db       1626 CAGTGACGCAGATATAAGTGAGCCCAAACGGGTGCGCGAGTCAGTTGCGCAGCCATCGAC 1685

Qy       1870 GTCAGACGCGGAAGGAGCTCCGGTGGACTTTGCCGACAGGTACCAAAACAAATGTTCTCG 1929
              ||||||||||||   |||| || |  ||| || ||||||||||||||||||||||||||
Db       1686 GTCAGACGCGGA---AGCTTCGATCAACTACGCAGACAGGTACCAAAACAAATGTTCTCG 1742

Qy       1930 TCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAAACATGCGAGAGAATGAATCAGAA 1989
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1743 TCACGCGGGCATGCTTCAGATGCTGTTTCCCTGCAAGACATGCGAGAGAATGAATCAGAA 1802

Qy       1990 TTTCAACATTTGCTTCACGCACGGGACCAGAGACTGTTCAGAATGTTTCCCCGGCGTGTC 2049
              |||||||||||||||||||||||||||| |||||||||||||| || ||||||||||||||
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Db      1803 TTTCAACATTTGCTTCACGCACGGGACGAGAGACTGTTCAGAGTGCTTCCCCGGCGTGTC 1862

Qy      2050 AGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCATTCATCATCT 2109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1863 AGAATCTCAACCGGTCGTCAGAAAGAGGACGTATCGGAAACTCTGTGCCATTCATCATCT 1922

Qy      2110 GCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGTGGATCTGGA 2169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1923 GCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGTGGACCTGGA 1982

Qy      2170 TGACTGTGTTTCTGAGCAATAAATGACTTAAACCAGGTATGGCTGCCGATGGTTATCTTC 2229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1983 TGACTGTGTTTCTGAGCAATAAATGACTTAAACCAGGTATGGCTGCCGATGGTTATCTTC 2042

Qy      2230 CAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGGCAGTGGTGGGACTTGAAACCTG 2289
             |||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db      2043 CAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGGACTTGAAACCTG 2102

Qy      2290 GAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTCTGGTGCTTC 2349
             |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2103 GAGCCCCGAAGCCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTCTGGTGCTTC 2162

Qy      2350 CTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCGTCAACGCGG 2409
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2163 CTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCGTCAACGCGG 2222

Qy      2410 CGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAGCGGGTGACA 2469
             |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2223 CGGACGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAGCGGGTGACA 2282

Qy      2470 ATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATA 2529
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2283 ATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATA 2342

Qy      2530 CGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGAGGGTTCTCGAAC 2589
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      2343 CGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGCGGGTTCTCGAAC 2402

Qy      2590 CTTTTGGTCTGGTTGAGGAAGGTGCTAAGACGGCTCCTGGAAAGAAACGTCCGGTAGAGC 2649
             || | |||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db      2403 CTCTCGGTCTGGTTGAGGAAGGCGCTAAGACGGCTCCTGGAAAGAAACGTCCGGTAGAGC 2462

Qy      2650 AGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGCAGCCCGCTA 2709
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2463 AGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATCGGCAAGACAGGCCAGCAGCCCGCTA 2522

Qy      2710 AAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGACCCACAACCTC 2769
             |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      2523 AAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGATCCACAACCTC 2582

Qy      2770 TCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGTG 2829
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2583 TCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGTG 2642

Qy      2830 GCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCTCAGGAAATT 2889
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2643 GCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCTCAGGAAATT 2702

Qy      2890 GGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCCGAACATGGG 2949
             |||||||||||||||||||||||||||||||||||||||||||||||||| || ||||||
Db      2703 GGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCCGCACCTGGG 2762

Qy      2950 CCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAACGGGGGCCA 3009
             |||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||
Db      2763 CCTTGCCCACCTACAATAACCACCTCTACAAGCAAATCTCCAGTGCTTCAACGGGGGCCA 2822

Qy      3010 GCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATTTCAACAGAT 3069
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2823 GCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATTTCAACAGAT 2882

Qy      3070 TCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATTGGGGATTCC 3129
             |||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||
Db      2883 TCCACTGCCACTTTTCACCACGTGACTGGCAGCGACTCATCAACAACAATTGGGGATTCC 2942
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Qy      3130 GGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCACGACGAATG 3189
             |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      2943 GGCCCAAGAGACTCAACTTCAAACTCTTCAACATCCAAGTCAAGGAGGTCACGACGAATG 3002

Qy      3190 ATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTGTCGGACTCGG 3249
             |||||||||| |||||||||||||||||||||||||||||||||||| ||||||||||
Db      3003 ATGGCGTCACAACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTCTCGGACTCGG 3062

Qy      3250 AGTACCAGTTCCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTCCGTTCCCGG 3309
             |||||||| | ||||||||||||||||||||||||||||||||||||||||||||||||
Db      3063 AGTACCAGCTTCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTCCGTTCCCGG 3122

Qy      3310 CGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCAGCCAGGCAG 3369
             |||||||||||||||||||| |||||||||| |||||||||||||||||||| || |
Db      3123 CGGACGTGTTCATGATTCCGCAATACGGCTACCTGACGCTCAACAATGGCAGCCAAGCCG 3182

Qy      3370 TGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGAGAACGGGCA 3429
             ||||||| |||||||||||||||||||||||||| || ||||||||||||||||||||
Db      3183 TGGGACGTTCATCCTTTTACTGCCTGGAATATTTCCCTTCTCAGATGCTGAGAACGGGCA 3242

Qy      3430 ATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACGCGCACA 3489
             | |||||||||||||||||||||| ||||| ||||||||||||||||||||||||||||
Db      3243 ACAACTTTACCTTCAGCTACACCTTTGAGGAAGTGCCTTTCCACAGCAGCTACGCGCACA 3302

Qy      3490 GCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATTACCTGAACA 3549
             |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db      3303 GCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAATACCTGTATTACCTGAACA 3362

Qy      3550 GAACTCACAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCCGTGGGTCTC 3609
             ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3363 GAACTCAAAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCCGTGGGTCTC 3422

Qy      3610 CAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACCGGCAGCAGC 3669
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      3423 CAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTATCGGCAGCAGC 3482

Qy      3670 GCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTGGTGCTTCAA 3729
             |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db      3483 GCGTTTCTAAAACAAAAACAGACAACAACAACAGCAATTTTACCTGGACTGGTGCTTCAA 3542

Qy      3730 AATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGGCCTCACACA 3789
             |||||||||| |||||||||||||| || ||||||||||||||||||||||||||||||
Db      3543 AATATAACCTCAATGGGCGTGAATCCATCATCAACCCTGGCACTGCTATGGCCTCACACA 3602

Qy      3790 AAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAAAGGAGAGCG 3849
             |||||||| |||||||||||||||||||||||||||||||||||||||| |||||||||
Db      3603 AAGACGACGAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAAAAGAGAGCG 3662

Qy      3850 CCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGGAAATCAAAG 3909
             |||||||||||||||||||||||||||||||||||||||||||| |||||||||||| ||||
Db      3663 CCGGAGCTTCAAACACTGCATTGGACAATGTCATGATTACAGACGAAGAGGAAATTAAAG 3722

Qy      3910 CCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCCAGAGCAGCA 3969
             |||||||||| |||||||||||||||||||||||| |||||||||||| ||||||||||||
Db      3723 CCACTAACCCTGTGGCCACCGAAAGATTTGGGACCGTGGCAGTCAATTTCCAGAGCAGCA 3782

Qy      3970 GCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAATGGTGTGGC 4029
             |||||||||||||||||||||||||||||||||||| |||||||| |||||||| ||||||
Db      3783 GCACAGACCCTGCGACCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGC 3842

Qy      4030 AAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACACGGATGGAC 4089
             |||| |||||||| |||||||||||||| |||||||||||||||||||||| |||||||
Db      3843 AAGATAGAGACGTGTACCTGCAGGGTCCCATTTGGGCCAAAATTCCTCACACAGATGGAC 3902

Qy      4090 ACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTCCTCAGATCC 4149
             |||||||||||||||||| |||||||||||||||| ||| ||||||||||||||||||||
Db      3903 ACTTTCACCCGTCTCCTCTTATGGGCGGCTTTGGACTCAAGAACCCGCCTCCTCAGATCC 3962

Qy      4150 TCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTACAAAGTTTG 4209
             |||||||||||||||||||||||||||||||||||||||||||| |||||||| ||||||||||
Db      3963 TCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCGGAGTTTTCAGCTACAAAGTTTG 4022
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Qy       4210 CTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAATGGGAGCTGC 4269
             |||||||||||||||| || |||||||||||||||||| ||||| ||||||||||||||||
Db       4023 CTTCATTCATCACCCAATACTCCACAGGACAAGTGAGTGTGGAAATTGAATGGGAGCTGC 4082

Qy       4270 AGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACTATGCAAAAT 4329
             |||||||||||||||| ||||||||||||||||||||||| ||||| || ||||||||||
Db       4083 AGAAAGAAAACAGCAAGCGCTGGAATCCCGAAGTGCAGTACACATCCAATTATGCAAAAT 4142

Qy       4330 CTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTCGCCCCATTG 4389
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       4143 CTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTATACTGAGCCTCGCCCCATTG 4202

Qy       4390 GCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCGGTTAATTCG 4449
             |||||||||||||| |||||||||||||||||  ||||||||||||||||||||| |||||
Db       4203 GCACCCGTTACCTTACCCGTCCCCTGTAATTACGTGTTAATCAATAAACCGGTTGATTCG 4262

Qy       4450 TGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCACCATAGCAACCGGT 4509
             | ||||||||||||||||||| ||||||| |||||||||  ||| ||||| |  |  | ||
Db       4263 TTTCAGTTGAACTTTGGTCTCCTGTCCTTCTTATCTTATC-GGTTACCATGGTTATAGCT 4321

Qy       4510 TACACATTAACTGCTTAGTTGCGCTT 4535
             |||||||||||||||| |||||||||
Db       4322 TACACATTAACTGCTTGGTTGCGCTT 4347


RESULT 12
AEF81093
ID   AEF81093 standard; DNA; 4347 BP.
XX
AC   AEF81093;
XX
DT   06-APR-2006  (first entry)
XX
DE   Adeno-associated virus related rep2cap1 DNA SEQ ID NO 1.
XX
KW   growth; food; meat; rep2cap1; ds.
XX
OS   Adeno-associated virus.
XX
PN   CN1626652-A.
XX
PD   15-JUN-2005.
XX
PF   08-DEC-2003; 2003CN-01117208.
XX
PR   08-DEC-2003; 2003CN-01117208.
XX
PA   (ZHEN-) ZHENGYANG GENE TECH CO LTD BENYUAN.
XX
PI   Dong X;
XX
DR   WPI; 2005-749951/77.
XX
PT   Method for accelerating quick growth of animals and method for improving
PT   quality of meat.
XX
PS   Disclosure; SEQ ID NO 1; 28pp; Chinese.
XX
CC   The invention relates to a method for promoting fast growth of animal and
CC   improving its meat quality features that the adenovirus associated virus
CC   carrier, especially the type-A one, is introduced to the growth hormone
CC   gene or relative gene. The present sequence represents an adeno-
CC   associated virus related rep2cap1 DNA.
XX
SQ   Sequence 4347 BP; 1106 A; 1186 C; 1142 G; 913 T; 0 U; 0 Other;

  Query Match             81.2%;  Score 3802;  DB 14;  Length 4347;
  Best Local Similarity   92.6%;  Pred. No. 0;
  Matches 4026;  Conservative    0;  Mismatches  315;  Indels    5;  Gaps    3;

Qy        191 GTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCATGTGGTCACGC 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 GTCCTGTATTAGAGGTCACGTGAGTGTTTTGCGACATTTTGCGACACCATGTGGTCACGC 65

Qy        251 TGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGAGGTTTGAACG 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 TGGGTATTTAAGCCCGAGTGAGCACGCAGGGTCTCCATTTTGAAGCGGGAGGTTTGAACG 125

Qy        311 CGCAG-CGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGACCTTGACGA 369
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CGCAGCCGCCATGCCGGGGTTTTACGAGATTGTGATTAAGGTCCCCAGCGACCTTGACGG 185

Qy        370 GCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGAATGGGAGTT 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GCATCTGCCCGGCATTTCTGACAGCTTTGTGAACTGGGTGGCCGAGAAGGAATGGGAGTT 245

Qy        430 GCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGACCGTGGCCGA 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GCCGCCAGATTCTGACATGGATCTGAATCTGATTGAGCAGGCACCCCTGACCGTGGCCGA 305

Qy        490 GAAGCTGCAGCGCGACTTCCTGGTCCACTGGCGCCGCGTGAGTAAGGCCCCGGAGGCCCT 549
              |||||||||||||||||| |||     | |||||||| ||||||||||||||||||||||
Db        306 GAAGCTGCAGCGCGACTTTCTGACGGAATGGCGCCGTGTGAGTAAGGCCCCGGAGGCCCT 365

Qy        550 CTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCTACTTCCACCTCCATATTCTGGTGGAGAC 609
              ||||||| || || |||||||| |||  |||||||||| | ||  | || ||||| ||
Db        366 TTTCTTTGTGCAATTTGAGAAGGGAGAGAGCTACTTCCACATGCACGTGCTCGTGGAAAC 425

Qy        610 CACGGGGGTCAAATCCATGGTGCTGGGCCGCTTCCTGAGTCAGATTAGCGACAAGCTGGT 669
              ||| ||||| |||||||||||  |||| || ||||||||||||||| |||| || ||| |
Db        426 CACCGGGGTGAAATCCATGGTTTTGGGACGTTTCCTGAGTCAGATTCGCGAAAAACTGAT 485

Qy        670 GCAGACCATCTACCGCGGGATCGAGCCGACCCTGCCCAACTGGTTCGCGGTGACCAAGAC 729
              ||||  || |||||||||||||||||||  |||| |||||||||||||| || |||||
Db        486 TCAGAGAATTTACCGCGGGATCGAGCCGACTTTGCCAAACTGGTTCGCGGTCACAAAGAC 545

Qy        730 GCGTAATGGCGCCGGAGGGGGGAACAAGGTGGTGGACGAGTGCTACATCCCCAACTACCT 789
              | |||||||||||||| ||||||||||||||||||| ||||||||||||||||| ||| |
Db        546 CAGAAATGGCGCCGGAGGCGGGAACAAGGTGGTGGATGAGTGCTACATCCCCAATTACTT 605

Qy        790 CCTGCCCAAGACTCAGCCCGAGCTGCAGTGGGCGTGGACTAACATGGAGGAGTATATAAG 849
              || ||||| || ||||| ||||| |||||||||||||||||| |||||  |||||| ||||
Db        606 GCTCCCCAAAACCCAGCCTGAGCTCCAGTGGGCGTGGACTAATATGGAACAGTATTTAAG 665

Qy        850 CGCGTGTTTAAACCTGGCCGAGCGCAAACGGCTCGTGGCGCACGACCTGACCCACGTCAG 909
              ||| ||||| || ||  | ||||| |||||| | ||||||||  | |||||  |||||
Db        666 CGCCTGTTTGAATCTCACGGAGCGTAAACGGTTGGTGGCGCAGCATCTGACGCACGTGTC 725

Qy        910 CCAGACCCAGGAGCAGAACAAGGAGAATCTGAACCCCAATTCTGACGCGCCTGTCATCCG 969
              ||||| |||||||||||||| ||||||| ||| |||||||||| ||||| || ||| |
Db        726 GCAGACGCAGGAGCAGAACAAAGAGAATCAGAATCCCAATTCTGATGCGCCGGTGATCAG 785

Qy        970 GTCAAAAACCTCCGCACGCTACATGGAGCTGGTCGGGTGGCTGGTGGACCGGGGCATCAC 1029
              |||||||| || ||  | ||||||||||||||||||||| ||||||  ||| || ||
Db        786 ATCAAAAACTTCAGCCAGGTACATGGAGCTGGTCGGGTGGCTCGTGGACAAGGGGATTAC 845

Qy       1030 CTCCGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCGTACATCTCCTTCAACGCCGCCTC 1089
              ||| |||||||||||||||||||||||||||||| |||||||||||||| || |||||
Db        846 CTCGGAGAAGCAGTGGATCCAGGAGGACCAGGCCTCATACATCTCCTTCAATGCGGCCTC 905

Qy       1090 CAACTCGCGGTCCCAGATCAAGGCCGCTCTGGACAATGCCGGCAAGATCATGGCGCTGAC 1149
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Db        906 CAACTCGCGGTCCCAAATCAAGGCTGCCTTGGACAATGCGGGAAAGATTATGAGCCTGAC 965

Qy       1150 CAAATCCGCGCCCGACTACCTGGTAGGCCCCGCTCCGCCCGCCGACATTAAAACCAACCG 1209
              ||| |||| |||||||||||||| ||||      ||     | ||||||   | ||| ||
Db        966 TAAAACCGCCCCCGACTACCTGGTGGGCCAGCAGCCCGTGGAGGACATTTCCAGCAATCG 1025

Qy       1210 CATTTACCGCATCCTGGAGCTGAACGGCTACGACCCTGCCTACGCCGGCTCCGTCTTTCT 1269
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Qy       1270 CGGCTGGGCCCAGAAAAGGTTCGGAAAACGCAACACCATCTGGCTGTTTGGGCCGGCCAC 1329
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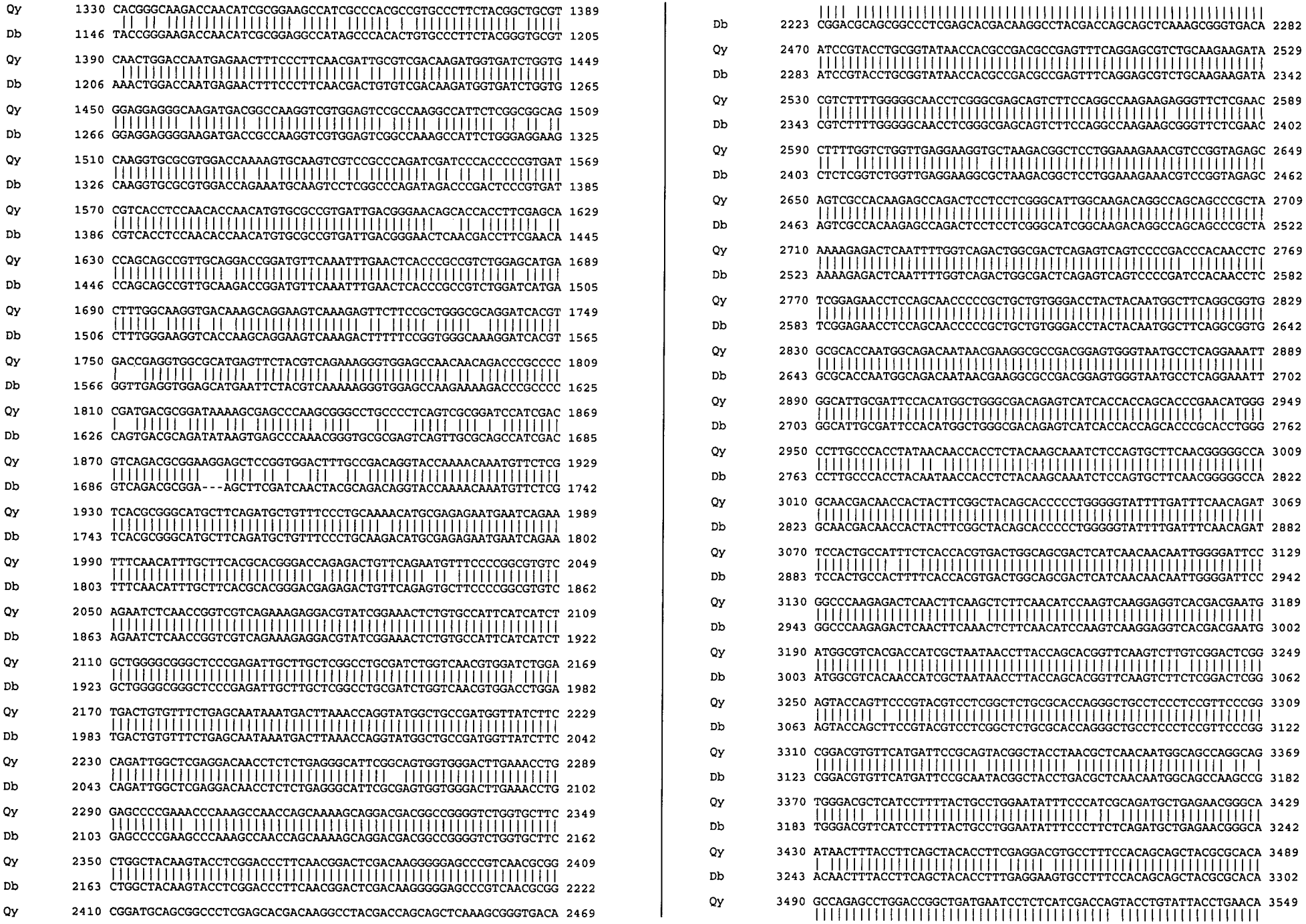
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Qy 1390 CAACTGGACCAATGAGAACTTTCCCTTCAACGATTGCGTCGACAAGATGGTGATCTGGTG 1449
Db 1206 AAACTGGACCAATGAGAACTTTCCCTTCAACGACTGTGTCGACAAGATGGTGATCTGGTG 1265
Qy 1450 GGAGGAGGGCAAGATGACGGCCAAGGTCGTGGAGTCCGCCAAGGCCATTCTCGGCGGCAG 1509
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Qy 1510 CAAGGTGCGCGTGGACCAAAAGTGCAAGTCGTCCGCCCAGATCGATCCCACCCCCGTGAT 1569
Db 1326 CAAGGTGCGCGTGGACCAGAAATGCAAGTCCTCGGCCCAGATAGACCCGACTCCCGTGAT 1385
Qy 1570 CGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACAGCACCACCTTCGAGCA 1629
Db 1386 CGTCACCTCCAACACCAACATGTGCGCCGTGATTGACGGGAACTCAACGACCTTCGAACA 1445
Qy 1630 CCAGCAGCCGTTGCAGGACCGGATGTTCAAATTTGAACTCACCCGCCGTCTGGAGCATGA 1689
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Qy 1690 CTTTGGCAAGGTGACAAAGCAGGAAGTCAAAGAGTTCTTCCGCTGGGCGCAGGATCACGT 1749
Db 1506 CTTTGGGAAGGTCACCAAGCAGGAAGTCAAAGACTTTTTCCGGTGGGCAAAGGATCACGT 1565
Qy 1750 GACCGAGGTGGCGCATGAGTTCTACGTCAGAAAGGGTGGAGCCAACAACAGACCCGCCCC 1809
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Qy 1810 CGATGACGCGGATAAAAGCGAGCCCAAGCGGGCCTGCCCCTCAGTCGCGGATCCATCGAC 1869
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Qy 1870 GTCAGACGCGGAAGGAGCTCCGGTGGACTTTGCCGACAGGTACCAAAACAAATGTTCTCG 1929
Db 1686 GTCAGACGCGGA---AGCTTCGATCAACTACGCAGACAGGTACCAAAACAAATGTTCTCG 1742
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Qy 2110 GCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGTGGATCTGGA 2169
Db 1923 GCTGGGGCGGGCTCCCGAGATTGCTTGCTCGGCCTGCGATCTGGTCAACGTGGACCTGGA 1982
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Db 1983 TGACTGTGTTTCTGAGCAATAAATGACTTAAACCAGGTATGGCTGCCGATGGTTATCTTC 2042
Qy 2230 CAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGGCAGTGGTGGGACTTGAAACCTG 2289
Db 2043 CAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGGACTTGAAACCTG 2102
Qy 2290 GAGCCCCGAAACCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTCTGGTGCTTC 2349
Db 2103 GAGCCCCGAAGCCCAAAGCCAACCAGCAAAAGCAGGACGACGGCCGGGGTCTGGTGCTTC 2162
Qy 2350 CTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCGTCAACGCGG 2409
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Qy 2410 CGGATGCAGCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAAGCGGGTGACA 2469
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Qy 2470 ATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATA 2529
Db 2283 ATCCGTACCTGCGGTATAACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATA 2342
Qy 2530 CGTCTTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAGAAGAGGGTTCTCGAAC 2589
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Db 2403 CTCTCGGTCTGGTTGAGGAAGGCGCTAAGACGGCTCCTGGAAAGAAACGTCCGGTAGAGC 2462
Qy 2650 AGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGCAGCCCGCTA 2709
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Qy 2770 TCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGTG 2829
Db 2583 TCGGAGAACCTCCAGCAACCCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGTG 2642
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Db 2643 GCGCACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCTCAGGAAATT 2702
Qy 2890 GGCATTGCGATTCCACATGGCTGGGCGACAGAGTCATCACCACCAGCACCCGAACATGGG 2949
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Qy 2950 CCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAACGGGGGCCA 3009
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Qy 3010 GCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATTTCAACAGAT 3069
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Qy 3070 TCCACTGCCATTTCTCACCACGTGACTGGCAGCGACTCATCAACAACAATTGGGGATTCC 3129
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Qy 3130 GGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAGTCAAGGAGGTCACGACGAATG 3189
Db 2943 GGCCCAAGAGACTCAACTTCAAACTCTTCAACATCCAAGTCAAGGAGGTCACGACGAATG 3002
Qy 3190 ATGGCGTCACGACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTGTCGGACTCGG 3249
Db 3003 ATGGCGTCACAACCATCGCTAATAACCTTACCAGCACGGTTCAAGTCTTCTCGGACTCGG 3062
Qy 3250 AGTACCAGTTCCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTCCGTTCCCGG 3309
Db 3063 AGTACCAGCTTCCGTACGTCCTCGGCTCTGCGCACCAGGGCTGCCTCCCTCCGTTCCCGG 3122
Qy 3310 CGGACGTGTTCATGATTCCGCAGTACGGCTACCTAACGCTCAACAATGGCAGCCAGGCAG 3369
Db 3123 CGGACGTGTTCATGATTCCGCAATACGGCTACCTGACGCTCAACAATGGCAGCCAAGCCG 3182
Qy 3370 TGGGACGCTCATCCTTTTACTGCCTGGAATATTTCCCATCGCAGATGCTGAGAACGGGCA 3429
Db 3183 TGGGACGTTCATCCTTTTACTGCCTGGAATATTTCCCTTCTCAGATGCTGAGAACGGGCA 3242
Qy 3430 ATAACTTTACCTTCAGCTACACCTTCGAGGACGTGCCTTTCCACAGCAGCTACGCGCACA 3489
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Qy 3490 GCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAGTACCTGTATTACCTGAACA 3549

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Db       3303 GCCAGAGCCTGGACCGGCTGATGAATCCTCTCATCGACCAATACCTGTATTACCTGAACA 3362

Qy       3550 GAACTCACAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCCGTGGGTCTC 3609
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3363 GAACTCAAAATCAGTCCGGAAGTGCCCAAAACAAGGACTTGCTGTTTAGCCGTGGGTCTC 3422

Qy       3610 CAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCCTGTTACCGGCAGCAGC 3669
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
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Qy       3670 GCGTTTCTAAAACAAAAACAGACAACAACAACAGCAACTTTACCTGGACTGGTGCTTCAA 3729
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       3483 GCGTTTCTAAAACAAAAACAGACAACAACAACAGCAATTTTACCTGGACTGGTGCTTCAA 3542

Qy       3730 AATATAACCTTAATGGGCGTGAATCTATAATCAACCCTGGCACTGCTATGGCCTCACACA 3789
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Db       3543 AATATAACCTCAATGGGCGTGAATCCATCATCAACCCTGGCACTGCTATGGCCTCACACA 3602

Qy       3790 AAGACGACAAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAAAGGAGAGCG 3849
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       3603 AAGACGACGAAGACAAGTTCTTTCCCATGAGCGGTGTCATGATTTTTGGAAAAGAGAGCG 3662

Qy       3850 CCGGAGCTTCAAACACTGCATTGGACAATGTCATGATCACAGACGAAGAGGAAATCAAAG 3909
              |||||||||||||||||||||||||||||||||| |||||||||||||||| ||||
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Qy       3910 CCACTAACCCCGTGGCCACCGAAAGATTTGGGACTGTGGCAGTCAATCTCCAGAGCAGCA 3969
              |||||||||| |||||||||||||||||||| |||||||||||| ||||||||||||
Db       3723 CCACTAACCCTGTGGCCACCGAAAGATTTGGGACCGTGGCAGTCAATTTCCAGAGCAGCA 3782

Qy       3970 GCACAGACCCTGCGACCGGAGATGTGCATGTTATGGGAGCCTTACCTGGAATGGTGTGGC 4029
              |||||||||||||||||||||||||||||||| ||||||||| |||||||| ||||||||||
Db       3783 GCACAGACCCTGCGACCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGC 3842

Qy       4030 AAGACAGAGACGTATACCTGCAGGGTCCTATTTGGGCCAAAATTCCTCACACGGATGGAC 4089
              |||| |||||||| |||||||||||||| |||||||||||||||||||||| |||||||
Db       3843 AAGATAGAGACGTGTACCTGCAGGGTCCCATTTGGGCCAAAATTCCTCACACAGATGGAC 3902

Qy       4090 ACTTTCACCCGTCTCCTCTCATGGGCGGCTTTGGACTTAAGCACCCGCCTCCTCAGATCC 4149
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Db       3903 ACTTTCACCCGTCTCCTCTTATGGGCGGCTTTGGACTCAAGAACCCGCCTCCTCAGATCC 3962

Qy       4150 TCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCAGAGTTTTCGGCTACAAAGTTTG 4209
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Db       3963 TCATCAAAAACACGCCTGTTCCTGCGAATCCTCCGGCGGAGTTTTCAGCTACAAAGTTTG 4022

Qy       4210 CTTCATTCATCACCCAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAATGGGAGCTGC 4269
              |||||||||||||||| || |||||||||||||||| ||||| ||||||||||||||||
Db       4023 CTTCATTCATCACCCAATACTCCACAGGACAAGTGAGTGTGGAAATTGAATGGGAGCTGC 4082

Qy       4270 AGAAAGAAAACAGCAAACGCTGGAATCCCGAAGTGCAGTATACATCTAACTATGCAAAAT 4329
              |||||||||||||||| |||||||||||||||||||||| ||||| || ||||||||||
Db       4083 AGAAAGAAAACAGCAAGCGCTGGAATCCCGAAGTGCAGTACACATCCAATTATGCAAAAT 4142

Qy       4330 CTGCCAACGTTGATTTCACTGTGGACAACAATGGACTTTATACTGAGCCTCGCCCCATTG 4389
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Db       4143 CTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTATACTGAGCCTCGCCCCATTG 4202

Qy       4390 GCACCCGTTACCTCACCCGTCCCCTGTAATTGTGTGTTAATCAATAAACCGGTTAATTCG 4449
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Db       4203 GCACCCGTTACCTTACCCGTCCCCTGTAATTACGTGTTAATCAATAAACCGGTTGATTCG 4262

Qy       4450 TGTCAGTTGAACTTTGGTCTCATGTCCTTATTATCTTATCTGGTCACCATAGCAACCGGT 4509
              | |||||||||||||||||| ||||||| |||||||||| ||| ||||| |  |  | |
Db       4263 TTTCAGTTGAACTTTGGTCTCCTGTCCTTCTTATCTTATC-GGTTACCATGGTTATAGCT 4321

Qy       4510 TACACATTAACTGCTTAGTTGCGCTT 4535
              |||||||||||||||| |||||||||
Db       4322 TACACATTAACTGCTTGGTTGCGCTT 4347


RESULT 13
ADE76502
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ID   ADE76502 standard; DNA; 4721 BP.
XX
AC   ADE76502;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Adeno-associated virus (AAV) related DNA, SEQ ID No 1.
XX
KW   adeno-associated virus; AAV; cytostatic; antipsoriatic; antirheumatic;
KW   antiarthritic; neuroprotective; antidiabetic; antithyroid;
KW   dermatological; antiinflammatory; gene therapy; vaccine;
KW   hyperproliferative; cancer; psoriasis; autoimmune disease;
KW   rheumatoid arthritis; multiple sclerosis; diabetes;
KW   autoimmune thyroiditis; scleroderma; Crohn's disease; gene; ds.
XX
OS   Adeno-associated virus 7.
XX
PN   EP1310571-A2.
XX
PD   14-MAY-2003.
XX
PF   12-NOV-2002; 2002EP-00257826.
XX
PR   13-NOV-2001; 2001US-0350607P.
PR   17-DEC-2001; 2001US-0341117P.
PR   01-MAY-2002; 2002US-0377066P.
PR   05-JUN-2002; 2002US-0386675P.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Gao G,  Wilson JM,  Alvira M;
XX
DR   WPI; 2003-450984/43.
DR   P-PSDB; ADE76503.
XX
PT   Detecting adeno-associated virus sequences in a sample, useful for e.g.
PT   preventing or treating hyperproliferative or autoimmune diseases,
PT   comprises subjecting a sample having a DNA to amplification via
PT   polymerase chain reaction.
XX
PS   Claim 17; SEQ ID NO 1; 419pp; English.
XX
CC   The invention relates to a novel method for detecting adeno-associated
CC   virus (AAV) sequences in a sample, which comprises subjecting a sample
CC   containing a DNA to amplification via a polymerase chain reaction (PCR).
CC   The AAV sequence have the following activities: cytostatic,
CC   antipsoriatic, antirheumatic, antiarthritic, neuroprotective,
CC   antidiabetic, antithyroid, dermatological, and antiinflammatory. The AAV
CC   sequence can be used in gene therapy or as part of a vaccine to treat
CC   disorders. The method is useful in detecting and/or identifying AAV
CC   sequences and isolating novel sequences that are identified. The
CC   sequences may be used e.g. for preventing or treating hyperproliferative
CC   conditions such as cancers and psoriasis, and other autoimmune diseases
CC   like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune
CC   thyroiditis, scleroderma or Crohn's disease. This polynucleotide sequence
CC   represents an AAV related DNA sequence of the invention.
XX
SQ   Sequence 4721 BP; 1108 A; 1405 C; 1301 G; 907 T; 0 U; 0 Other;

  Query Match             78.5%;  Score 3678.4;  DB 10;  Length 4721;
  Best Local Similarity   87.5%;  Pred. No. 0;
  Matches 4135;  Conservative    0;  Mismatches  541;  Indels   52;  Gaps    8;

Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
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Db          1 TTGGCCACTCCCTCTATGCGCGCTCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGC 60

Qy         61 CGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG 120
                |||| | | ||| ||| | | ||||| ||  |||||||||||||||| ||||||||||
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Qy        121 GCCAACTCCATCACTAGGGGTTCCTGGAGG----------------GGTGGAGTCGTGAC 164
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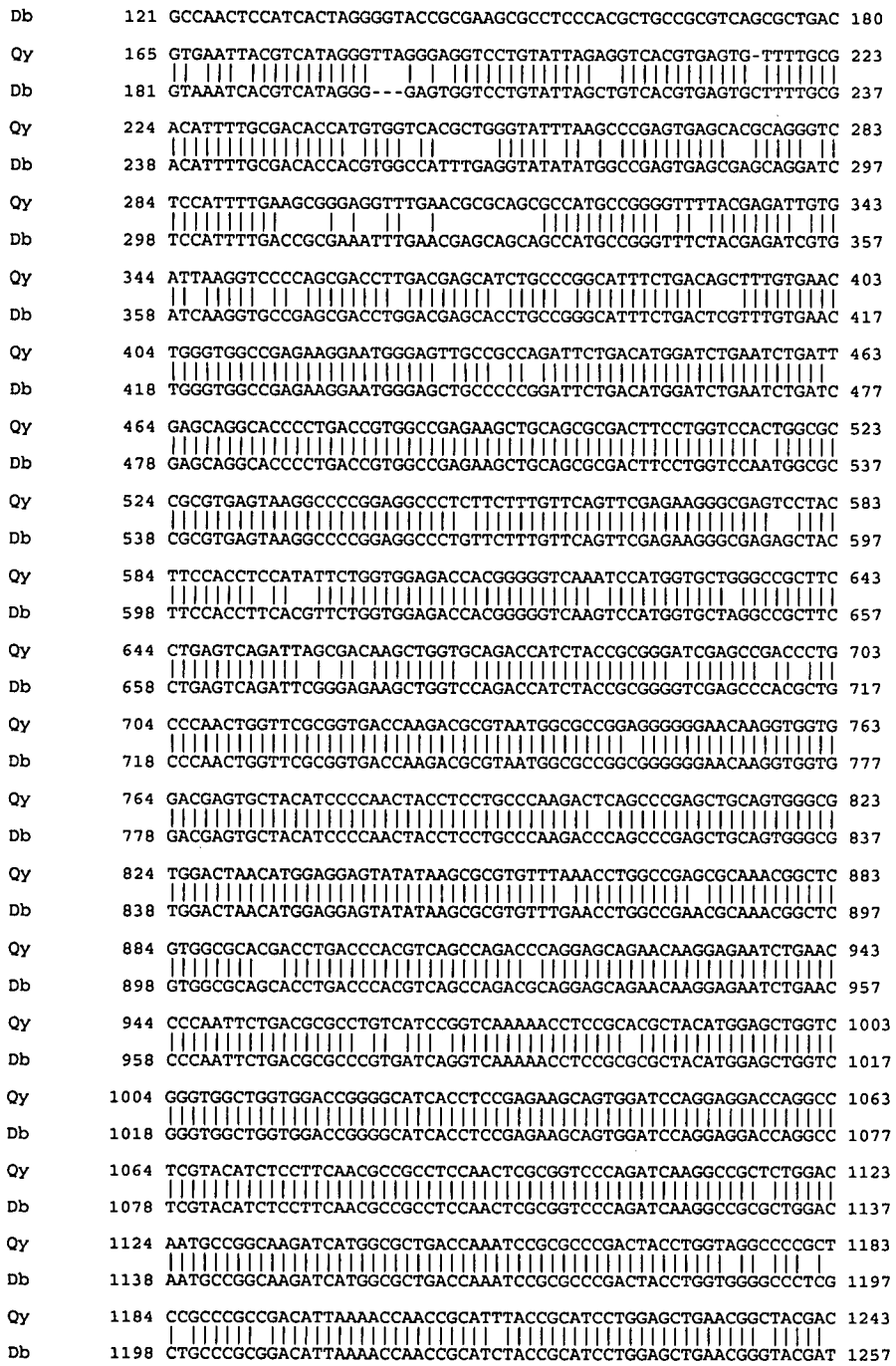

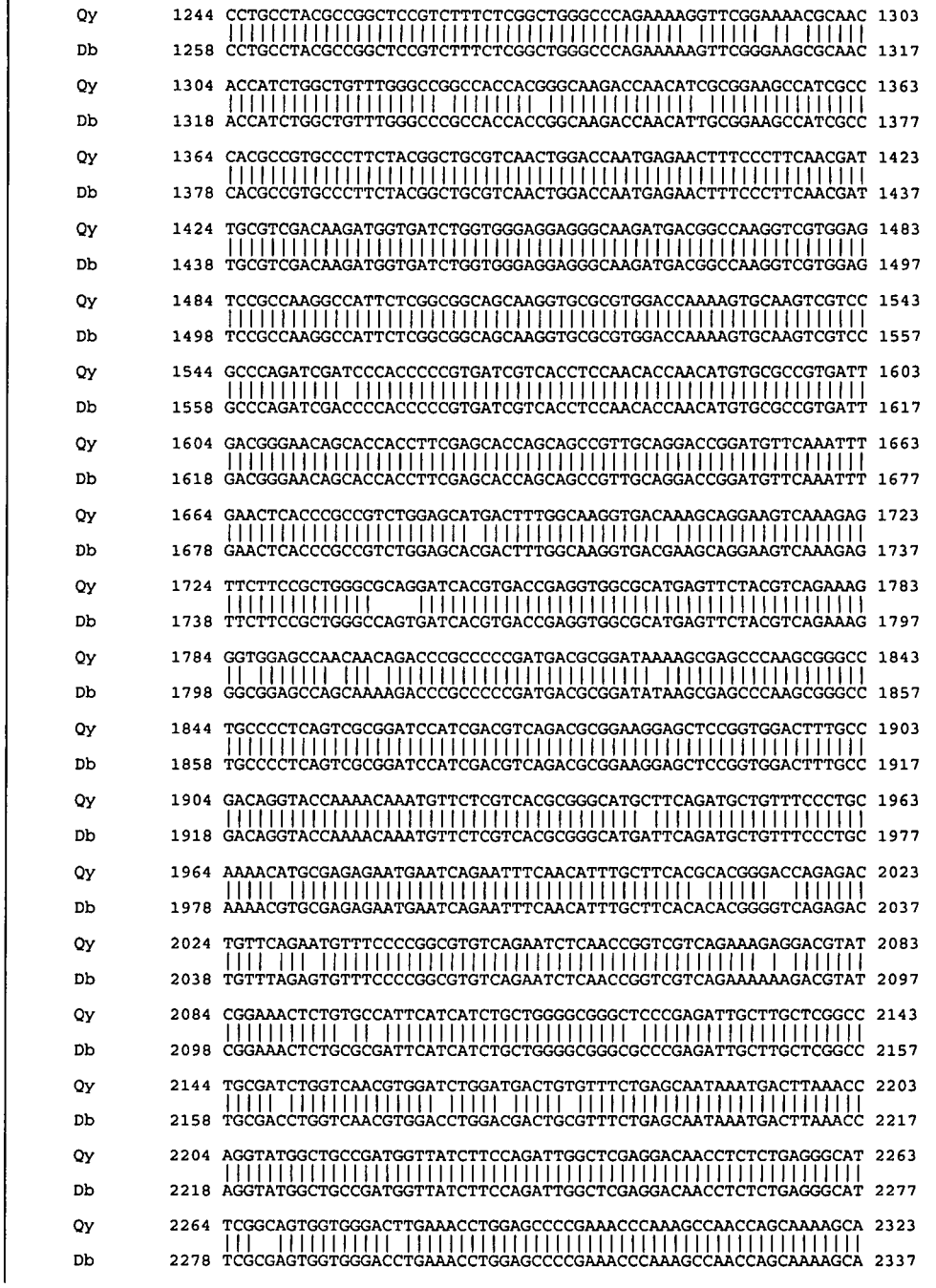

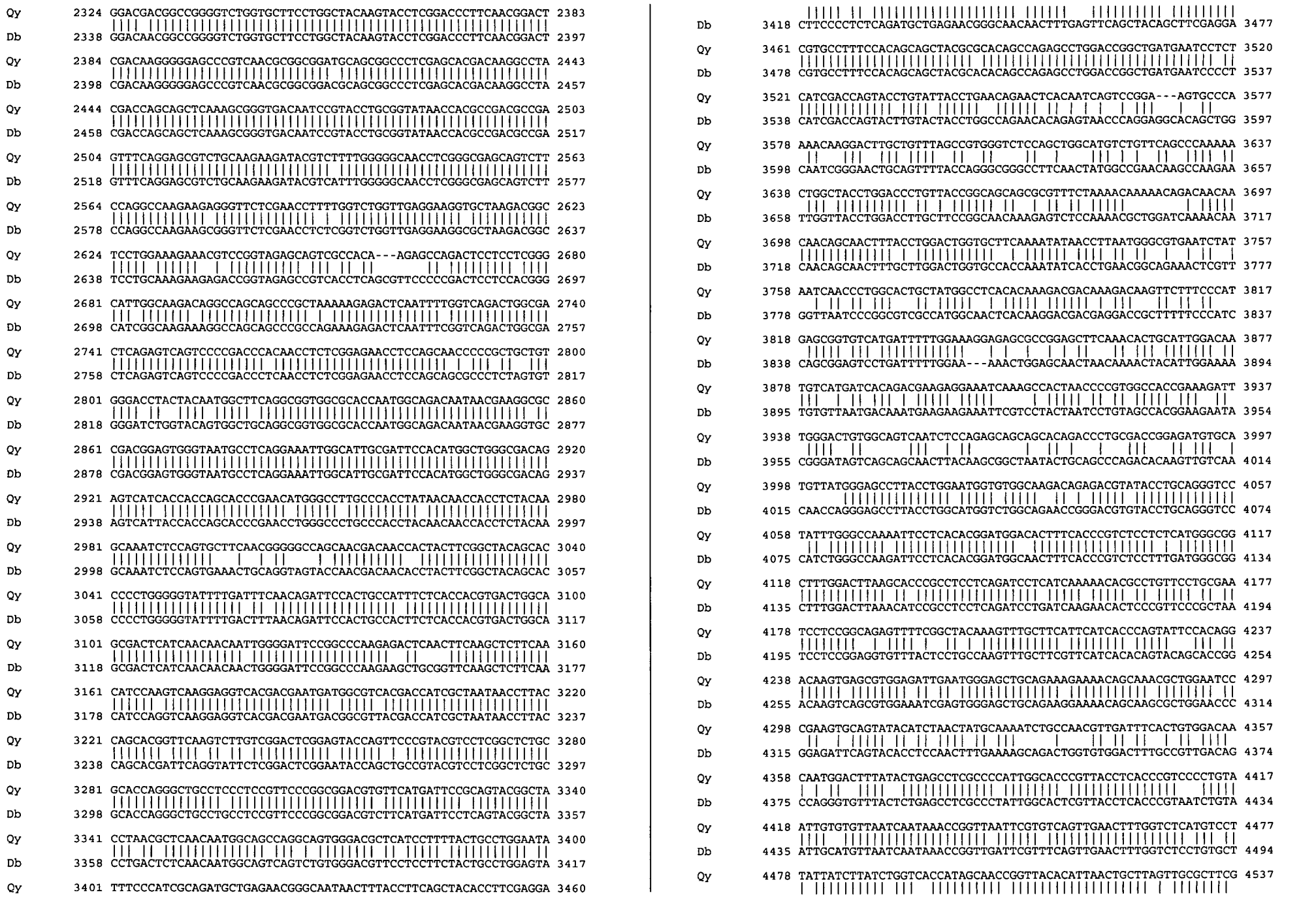

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              |||                      |||||||||||||||||||| ||||||||||||||
Db       4554 CGATAAGAACACTGACGTCACCGCGGTACCCCTAGTGATGGAGTTGGCCACTCCCTCTAT 4613

Qy       4576 GCGCGCTCGCTCGCTCGGTGGGGCCGGCAGAGCAGAGCTCTGCCGTCTGCGGACCTTTGG 4635
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Db       4614 GCGCGCTCGCTCGCTCGGTGGGGCCTGCGGACCAAAGGTCCGCAGACGGCAGAGCTCTGC 4673

Qy       4636 TCCGCAGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGCCAA 4683
              || || ||||||||||||||||||||||||||||||||||||||||||
Db       4674 TCTGCCGGCCCCACCGAGCGAGCGAGCGCGCATAGAGGGAGTGGCCAA 4721


RESULT 14
ADG39764
ID   ADG39764 standard; DNA; 4721 BP.
XX
AC   ADG39764;
XX
DT   11-MAR-2004  (first entry)
XX
DE   AAV-7 genomic DNA sequence SEQ ID NO:26.
XX
KW   parvovirus; rep; cap; DNA binding domain; capsid interacting domain;
KW   recombinant hybrid parvovirus particle;
KW   recombinant adeno-associated virus; rAAV; AAV; vaccine; gene therapy;
KW   gene; ds.
XX
OS   Adeno-associated virus 7.
XX
PN   WO2003104392-A2.
XX
PD   18-DEC-2003.
XX
PF   02-DEC-2002; 2002WO-US038423.
XX
PR   18-DEC-2001; 2001US-0341919P.
XX
PA   (UYNC-) UNIV NORTH CAROLINA.
XX
PI   Samulski RJ,  Rabinowitz JE;
XX
DR   WPI; 2004-062324/06.
XX
PT   New polynucleotides comprising parvovirus rep coding sequences and
PT   parvovirus cap coding sequences, useful in producing higher stocks of
PT   hybrid parvovirus vectors for delivering therapeutic nucleic acids to a
PT   subject.
XX
PS   Disclosure; SEQ ID NO 26; 115pp; English.
XX
CC   The present invention describes a polynucleotide (I), comprising
CC   parvovirus rep coding sequences and parvovirus cap coding sequences. The
CC   rep coding sequences encodes a DNA binding domain from a first
CC   parvovirus, and a capsid interacting domain from a parvovirus different
CC   from the first parvovirus. The cap coding sequence comprises sequences
CC   from the different parvovirus. Also described: (1) a vector comprising
CC   (I); (2) a cell comprising (I), or parvovirus rep coding sequences and
CC   parvovirus cap coding sequences, where the rep coding sequences encode a
CC   DNA binding domain from a first parvovirus and a capsid interacting
CC   domain from a parvovirus different from the first parvovirus, the cap
CC   coding sequences comprise sequences from the different parvovirus, and
CC   the rep coding sequences are stably integrated into the genome of the
CC   cell; and (3) producing a recombinant hybrid parvovirus particle or adeno
CC   -associated virus (rAAV) particle. (I) can be used in vaccines, and in
CC   gene therapy. The polynucleotide (I) can be used in producing higher
CC   stocks of hybrid parvoviruses or parvovirus vectors, which may be used in
CC   the delivery of nucleic acids having biological effect to treat or
CC   ameliorate the symptoms associated with any disorder related to gene
CC   expression. The polynucleotide may be used to produce a parvovirus vector
CC   to express an immunogenic polypeptide in a subject, e.g. for vaccination.
CC   The parvovirus vector may also be used to provide an antisense nucleic
CC   acid to a cell in vitro or in vivo, or in diagnostic and screening
CC   methods. The present sequence is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 4721 BP; 1108 A; 1405 C; 1301 G; 907 T; 0 U; 0 Other;

  Query Match            78.5%;  Score 3678.4;  DB 12;  Length 4721;
  Best Local Similarity  87.5%;  Pred. No. 0;
  Matches 4135;  Conservative    0;  Mismatches  541;  Indels   52;  Gaps    8;

Qy          1 TTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCC 60
              |||||||||||||||| ||||||||||||||||||  || |||| |  ||||||||||  |
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Qy        284 TCCATTTTGAAGCGGGAGGTTTGAACGCGCAGCGCCATGCCGGGGTTTTACGAGATTGTG 343
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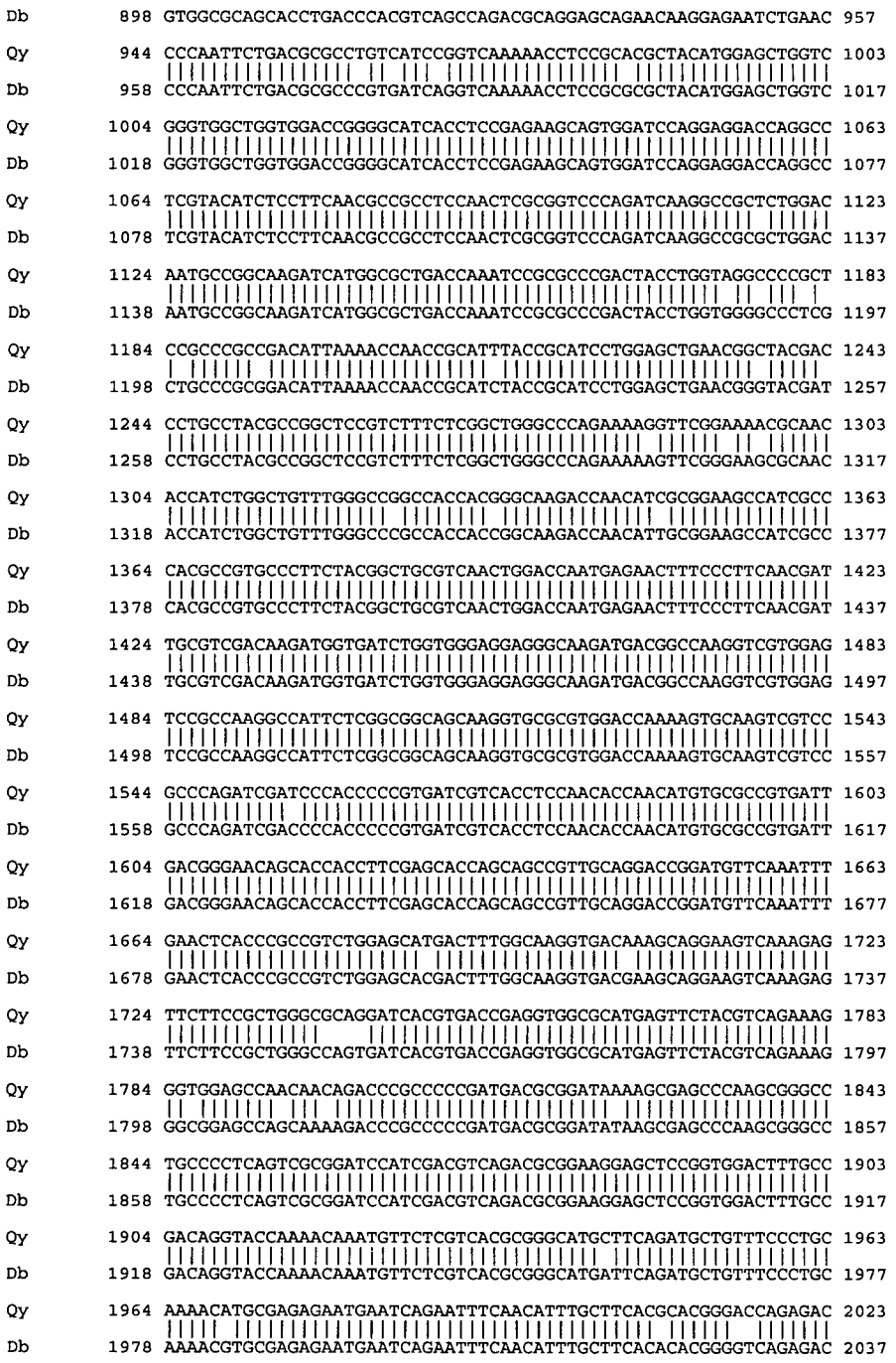
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XX
DT   10-MAR-2005  (first entry)
XX
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KW   apolipoprotein E; apoE; apolipoprotein A; apoA; atherosclerosis;
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XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Rader DJ, Wilson JM;
XX
DR WPI; 2005-031700/03.
XX
PT Lowering total cholesterol levels and treating atherosclerosis in a
PT subject comprises delivering a recombinant adeno-associated virus (AAV)
PT comprising an AAV serotype capsid protein or a gene encoding human
PT apolipoprotein E (apoE) or apoA.
XX
PS Disclosure; SEQ ID NO 7; 69pp; English.
XX
CC The specification describes a method for lowering total cholesterol
CC levels in a subject. The method comprises delivering to the subject a
CC recombinant adeno-associated virus (AAV) comprising a gene encoding a
CC human apolipoprotein E (apoE) or apoA under the control of a regulatory
CC control sequence which directs expression of the gene. The recombinant
CC AAV also comprises a capsid protein selected from an AAV serotype (e.g.
CC AAV7 or AAV8) which preferentially expresses high levels of transgene in
CC live. A therapeutically effective amount of apoE or apoA expression is
CC obtained upon delivery of low dose of AAV. The method of the invention is
CC useful for lowering total cholesterol levels in a subject, e.g. for
CC treating atherosclerosis, and for correcting defects in lipoprotein. The
CC present sequence represents AAV serotype 7 (AAV7), which may be used to
CC produce recombinant AAV vectors of the invention.
XX
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Query Match 78.5%; Score 3678.4; DB 14; Length 4721;
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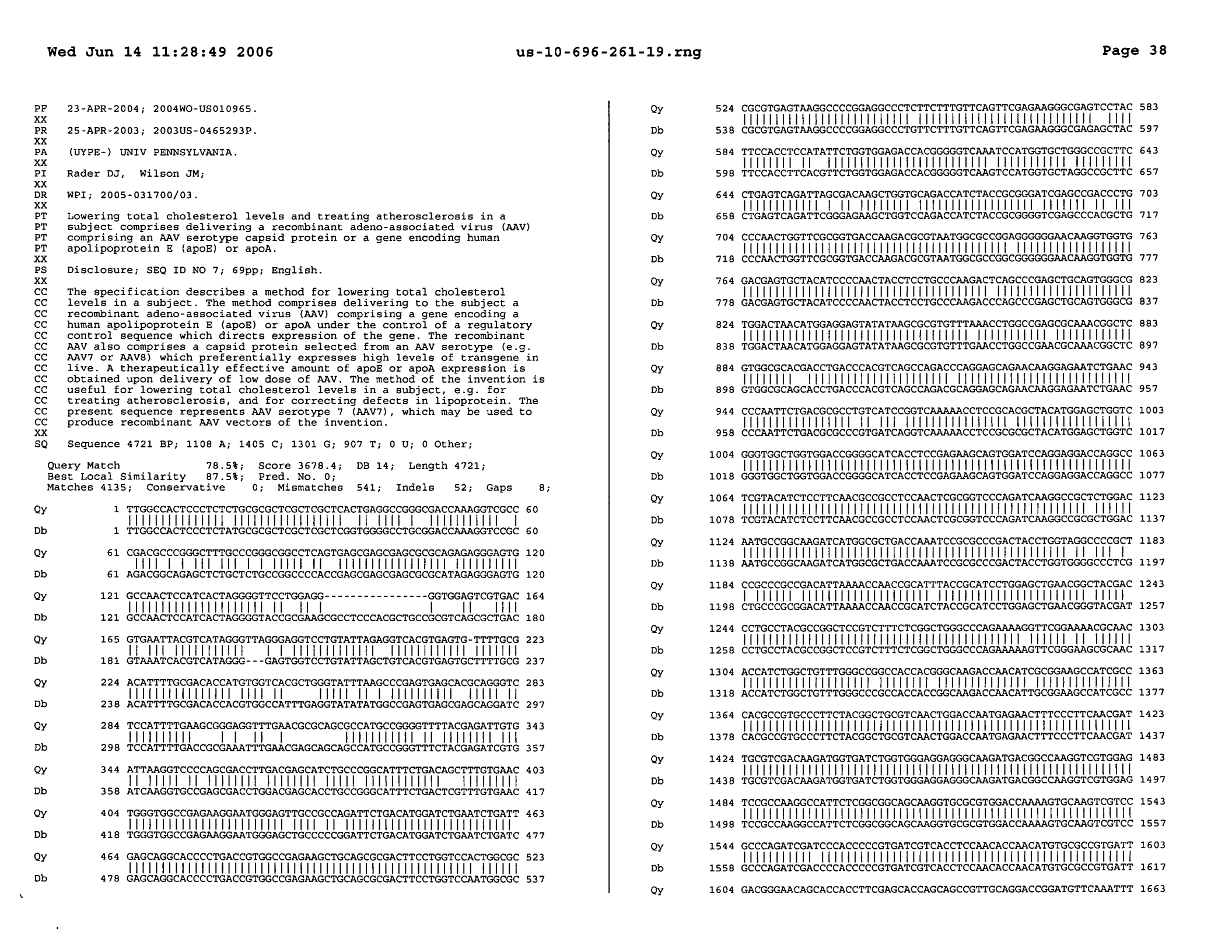

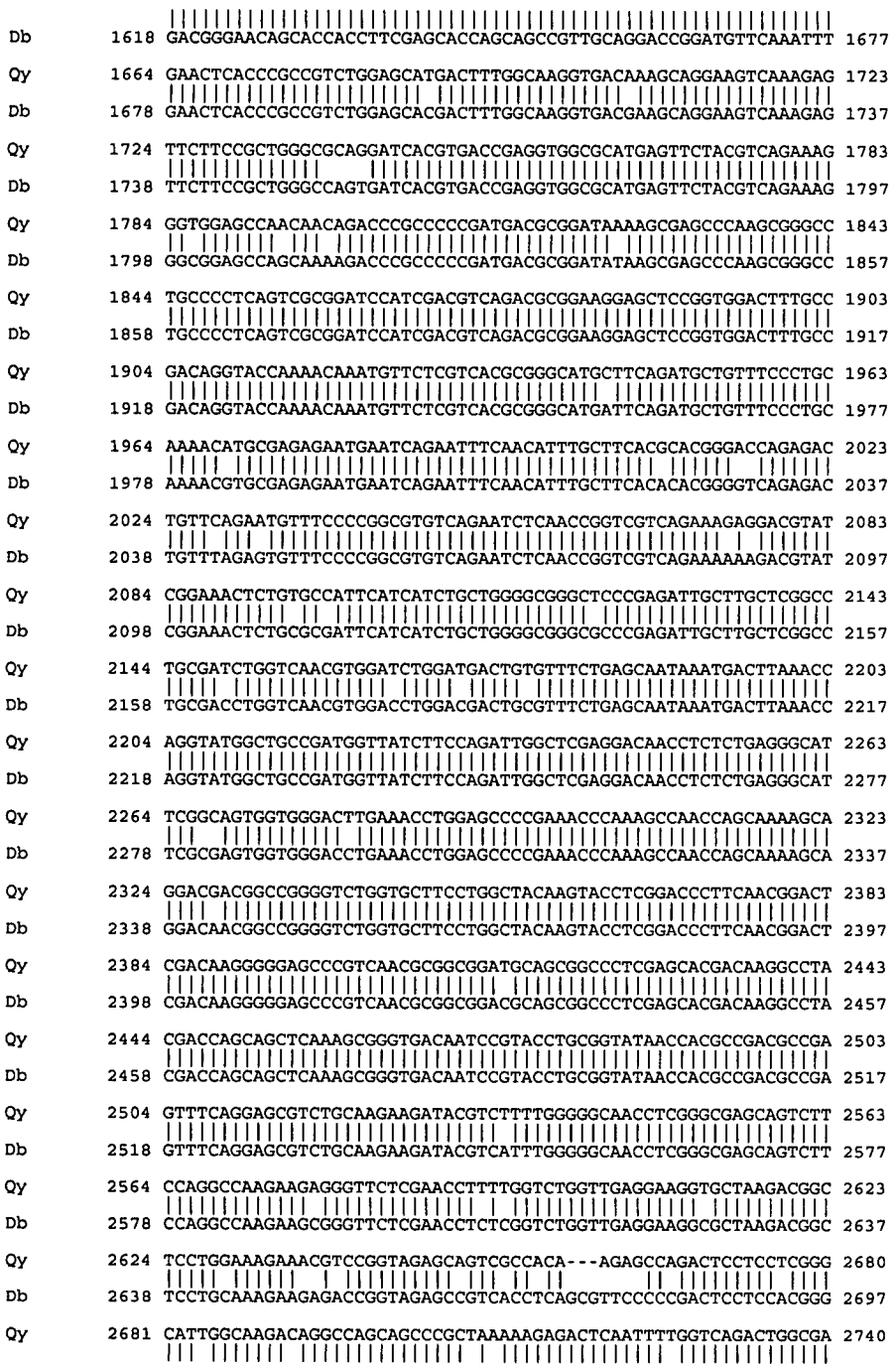
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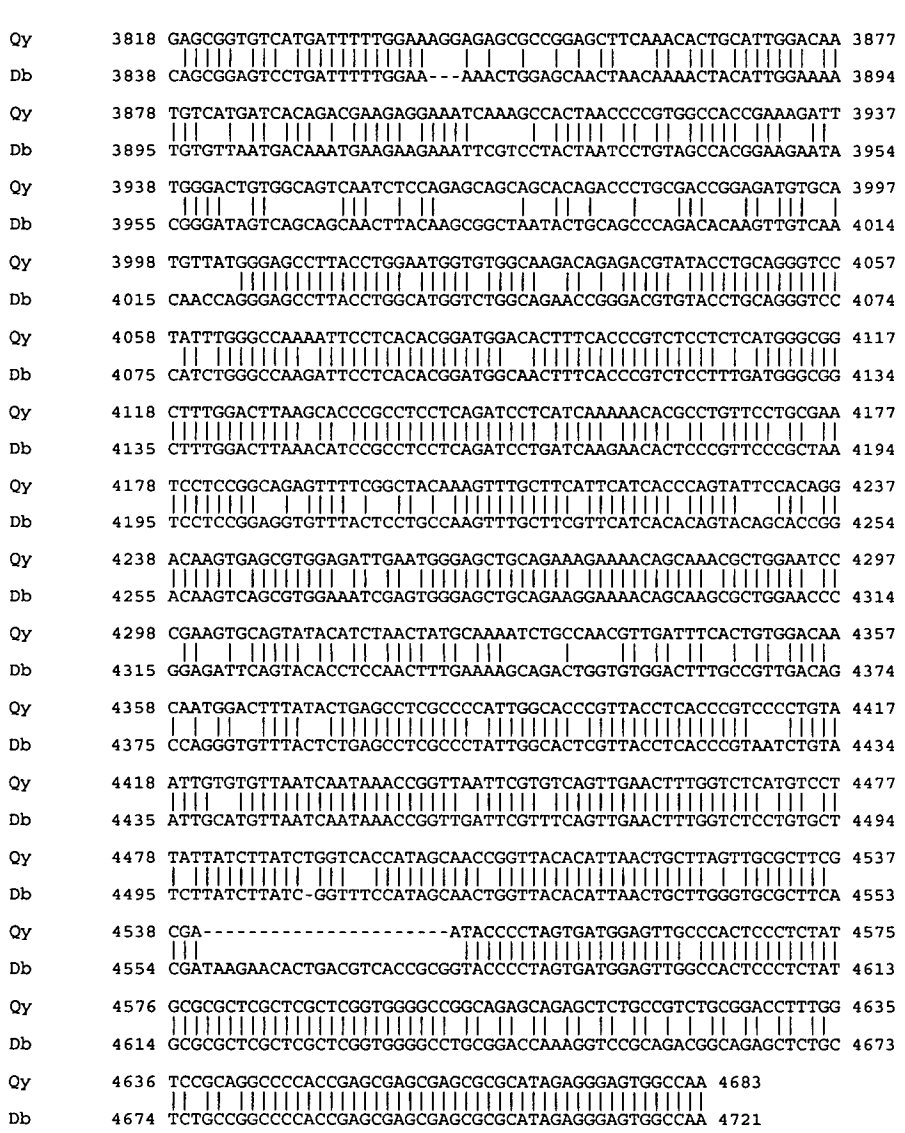

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Job time : 2697 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 12:43:06 ; Search time 25755 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4683	100.0	4683	2	AR562507	AR562507 Sequence
3	4663.8	99.6	4683	10	AF028704	AF028704 Adeno-ass
4	4253.2	90.8	4718	2	BD242766	BD242766 Adeno-ass
5	4253.2	90.8	4718	2	AR562498	AR562498 Sequence
6	4253.2	90.8	4718	2	AX753251	AX753251 Sequence
7	4253.2	90.8	4718	10	AF063497	AF063497 Adeno-ass
8	3678.4	78.5	4721	2	CQ972062	CQ972062 Sequence
9	3678.4	78.5	4721	2	CS073592	CS073592 Sequence
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ALIGNMENTS

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BD242775
LOCUS BD242775 4683 bp DNA linear PAT 17-JUL-2003
DEFINITION Adeno-associated virus serum type 1 nucleic acid sequence, vector and host cell containing the same.
ACCESSION BD242775
VERSION BD242775.1 GI:33052545
KEYWORDS JP 2002529098-A/10.
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
REFERENCE 1 (bases 1 to 4683)
AUTHORS Wilson,J.M. and Xiao,W.
TITLE Adeno-associated virus serum type 1 nucleic acid sequence, vector and host cell containing the same
JOURNAL Patent: JP 2002529098-A 10 10-SEP-2002;
THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
COMMENT OS aav-6
PN JP 2002529098-A/10
PD 10-SEP-2002
PF 02-NOV-1999 JP 2000581227
PR 05-NOV-1998 US 60/107114
PI JAMES M WILSON,WEIDONG XIAO
PC C12N15/09,A61K31/711,A61K48/00,A61P43/00,C12N1/15,C12N1/19, PC C12N1/21,
PC C12N5/10,C12P21/02//A61K35/76,C12N15/00,C12N5/00 CC
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CC cell containing the same
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/organism="unidentified"
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Query Match 100.0%; Score 4683; DB 2; Length 4683;
Best Local Similarity 100.0%; Pred. No. 0;

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Qy       2341 TGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAACGGACTCGACAAGGGGGAGCCCG 2400
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Qy       2641 CGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCGGGCATTGGCAAGACAGGCCAGC 2700
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Qy       2941 GAACATGGGCCTTGCCCACCTATAACAACCACCTCTACAAGCAAATCTCCAGTGCTTCAA 3000
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Qy       3001 CGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGATT 3060
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DEFINITION  Sequence 19 from patent US 6759237.
ACCESSION   AR562507
VERSION     AR562507.1  GI:53976573
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4683)
  AUTHORS   Wilson,J.M. and Xiao,W.
  TITLE     Adeno-associated virus serotype 1 nucleic acid sequences, vectors
            and host cells containing same
  JOURNAL   Patent: US 6759237-A 19 06-JUL-2004;
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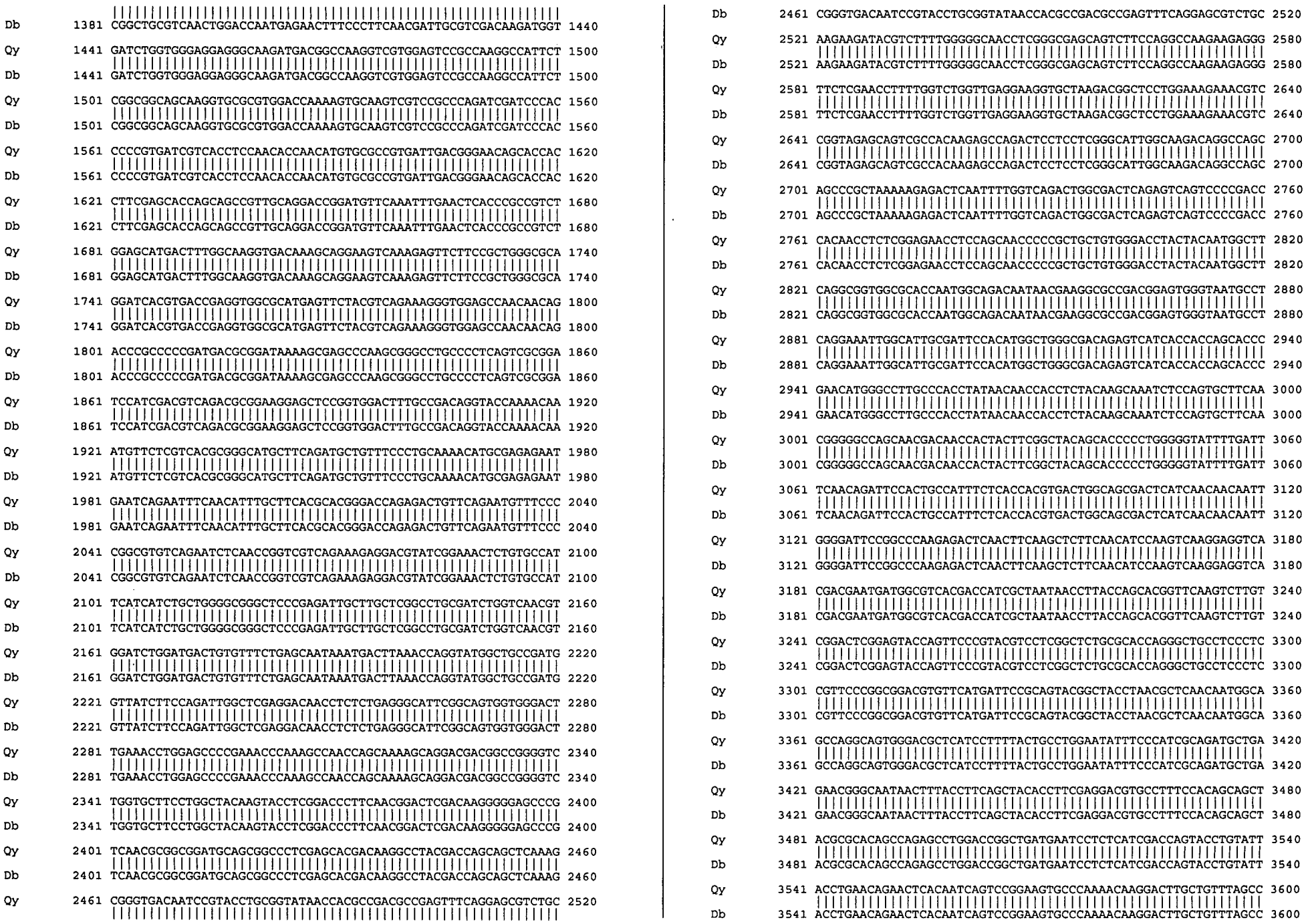
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Db       4681 CAA 4683
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RESULT 3
AF028704
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DEFINITION  Adeno-associated virus 6, complete genome.
ACCESSION   AF028704
VERSION     AF028704.1  GI:2766605
KEYWORDS    .
SOURCE      Adeno-associated virus 6
  ORGANISM  Adeno-associated virus 6
            Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.
REFERENCE   1  (bases 1 to 4683)
  AUTHORS   Rutledge,E.A., Halbert,C.L. and Russell,D.W.
  TITLE     Infectious clones and vectors derived from adeno-associated virus
            (AAV) serotypes other than AAV type 2
  JOURNAL   J. Virol. 72 (1), 309-319 (1998)
   PUBMED   9420229
REFERENCE   2  (bases 1 to 4683)
  AUTHORS   Rutledge,E.A. and Russell,D.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1997) Hematology, Univ. of Washington, Box
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ORIGIN

  Query Match             99.6%;  Score 4663.8;  DB 10;  Length 4683;
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 4671; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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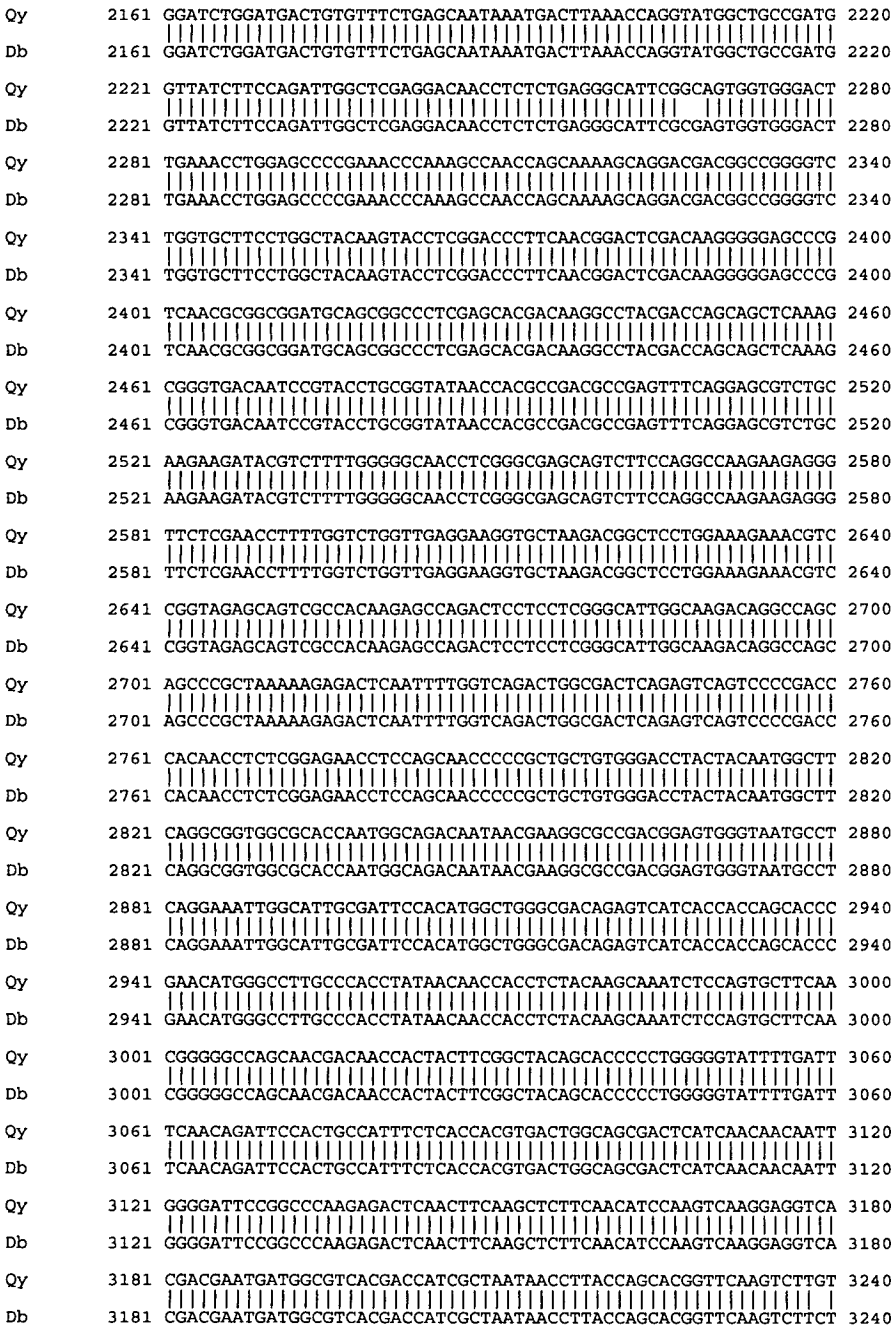
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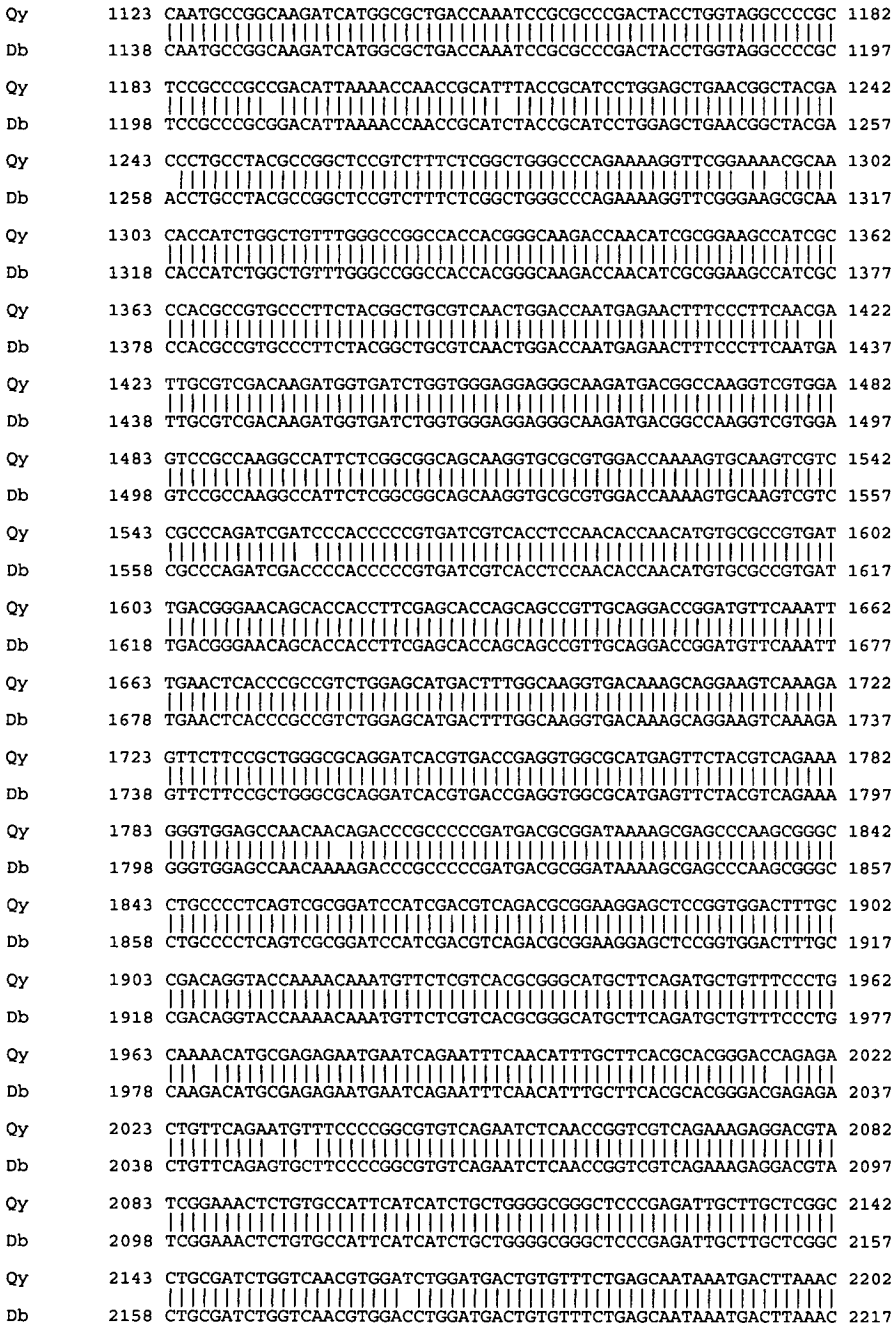
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VERSION AR562498.1 GI:53976564
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SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 4718)
AUTHORS Wilson,J.M. and Xiao,W.
TITLE Adeno-associated virus serotype 1 nucleic acid sequences, vectors and host cells containing same
JOURNAL Patent: US 6759237-A 1 06-JUL-2004;
The Trustees of the University of Pennsylvania; Philadelphia, PA
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Query Match 90.8%; Score 4253.2; DB 2; Length 4718;
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Qy        164 CGTGAATTACGTCATAGGGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTG-TTTTGC 222

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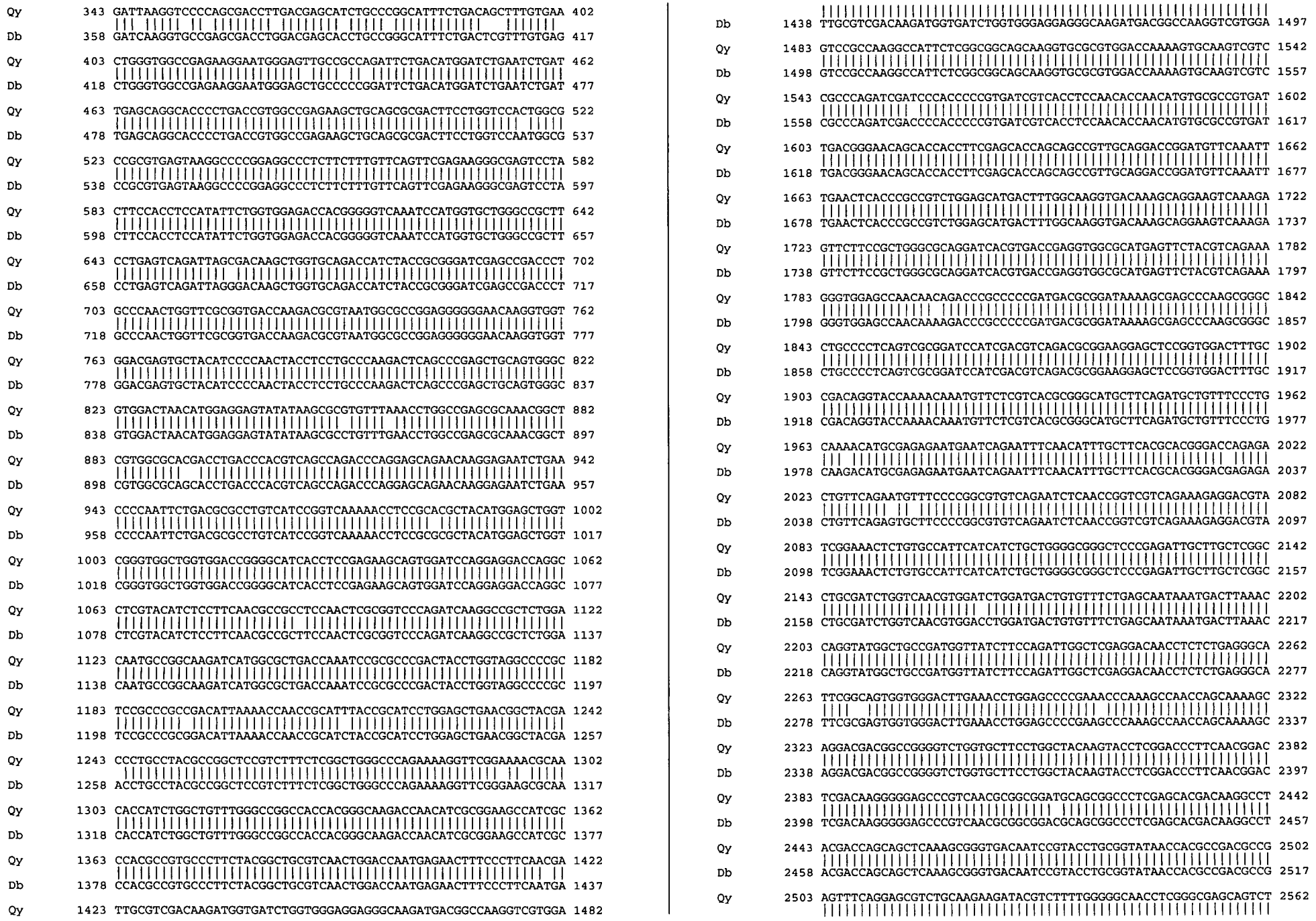

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ACCESSION   AX753251
VERSION     AX753251.1  GI:32166108
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REFERENCE   1
  AUTHORS   Gao,G., Wilson,J.M. and Alvira,M.
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  ORGANISM  Adeno-associated virus - 1
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  AUTHORS   Xiao,W., Chirmule,N., Berta,S.C., McCullough,B., Gao,G. and
            Wilson,J.M.
  TITLE     Gene therapy vectors based on adeno-associated virus type 1
  JOURNAL   J. Virol. 73 (5), 3994-4003 (1999)
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REFERENCE   2  (bases 1 to 4718)
  AUTHORS   Xiao,W. and Wilson,J.M.
  TITLE     Direct Submission
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ORIGIN

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RESULT 8

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ACCESSION   CQ972062
VERSION     CQ972062.1  GI:57163375
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  ORGANISM  Adeno-associated virus
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REFERENCE   1
  AUTHORS   Rader,D.J. and Wilson,J.M.
  TITLE     Methods and compositions for lowering total cholesterol levels and
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  JOURNAL   Patent: WO 2004108922-A 7 16-DEC-2004;
            The Trustees of The University of Pennsylvania (US)
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ORIGIN

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Qy        165 GTGAATTACGTCATAGGGTTAGGGAGGTCCTGTATTAGAGGTCACGTGAGTG-TTTTGCG 223
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Qy        224 ACATTTTGCGACACCATGTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCACGCAGGGTC 283
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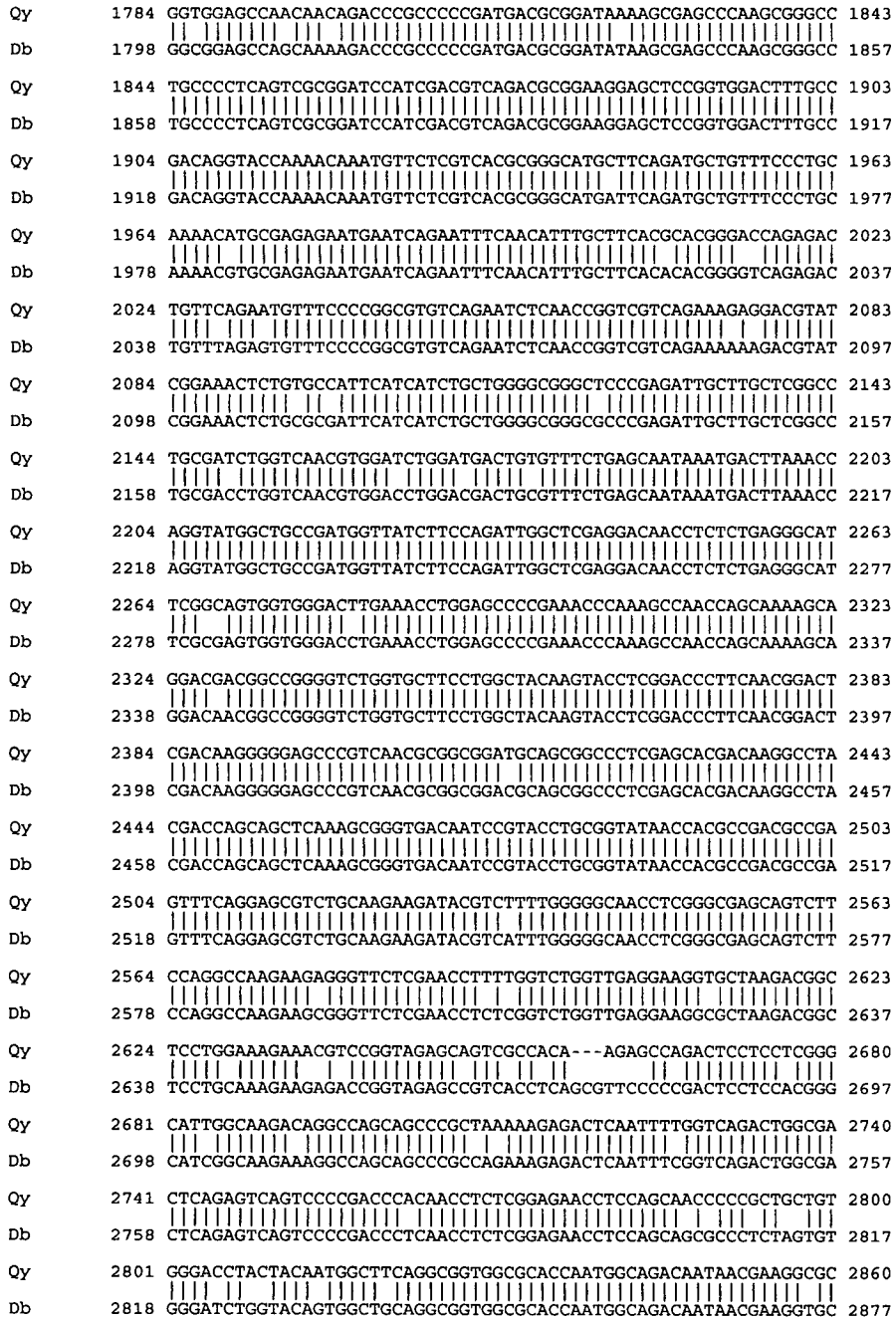
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  AUTHORS   Wilson,J.M., Gao,G., Alvira,M.R. and Vandenberghe,L.H.
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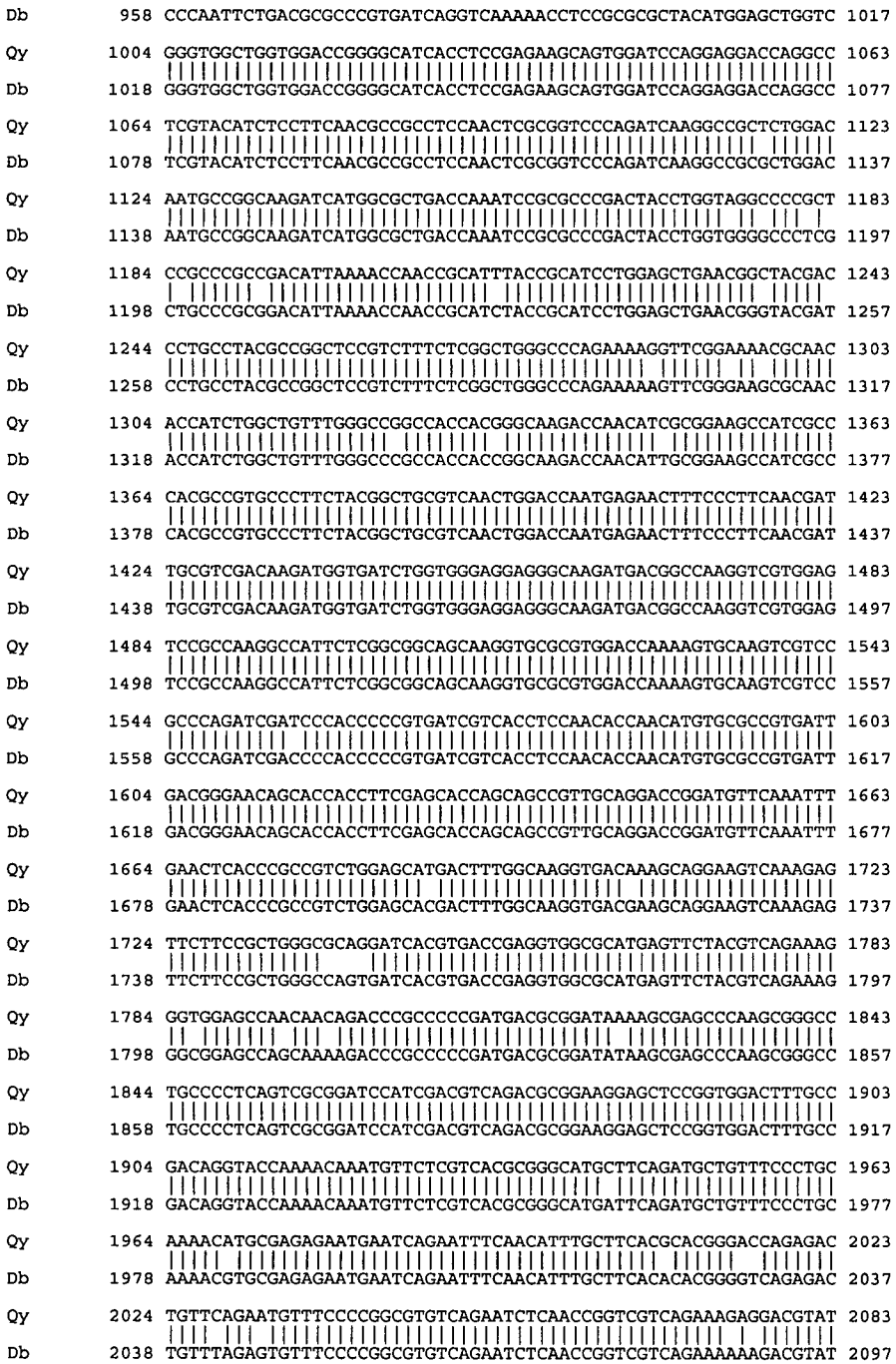
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LOCUS AX753246 4721 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 1 from Patent EP1310571.
ACCESSION AX753246
VERSION AX753246.1 GI:32166105
KEYWORDS .
SOURCE Adeno-associated virus - 7
ORGANISM Adeno-associated virus - 7
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus;
unclassified Dependovirus.
REFERENCE 1
AUTHORS Gao,G., Wilson,J.M. and Alvira,M.
TITLE A method of detecting and/or identifying adeno-associated virus
(AVV) sequences and isolating novel sequences identified thereby
JOURNAL Patent: EP 1310571-A 1 14-MAY-2003;
The Trustees of The University of Pennsylvania (US)
FEATURES Location/Qualifiers
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ORIGIN

Query Match 78.5%; Score 3678.4; DB 2; Length 4721;
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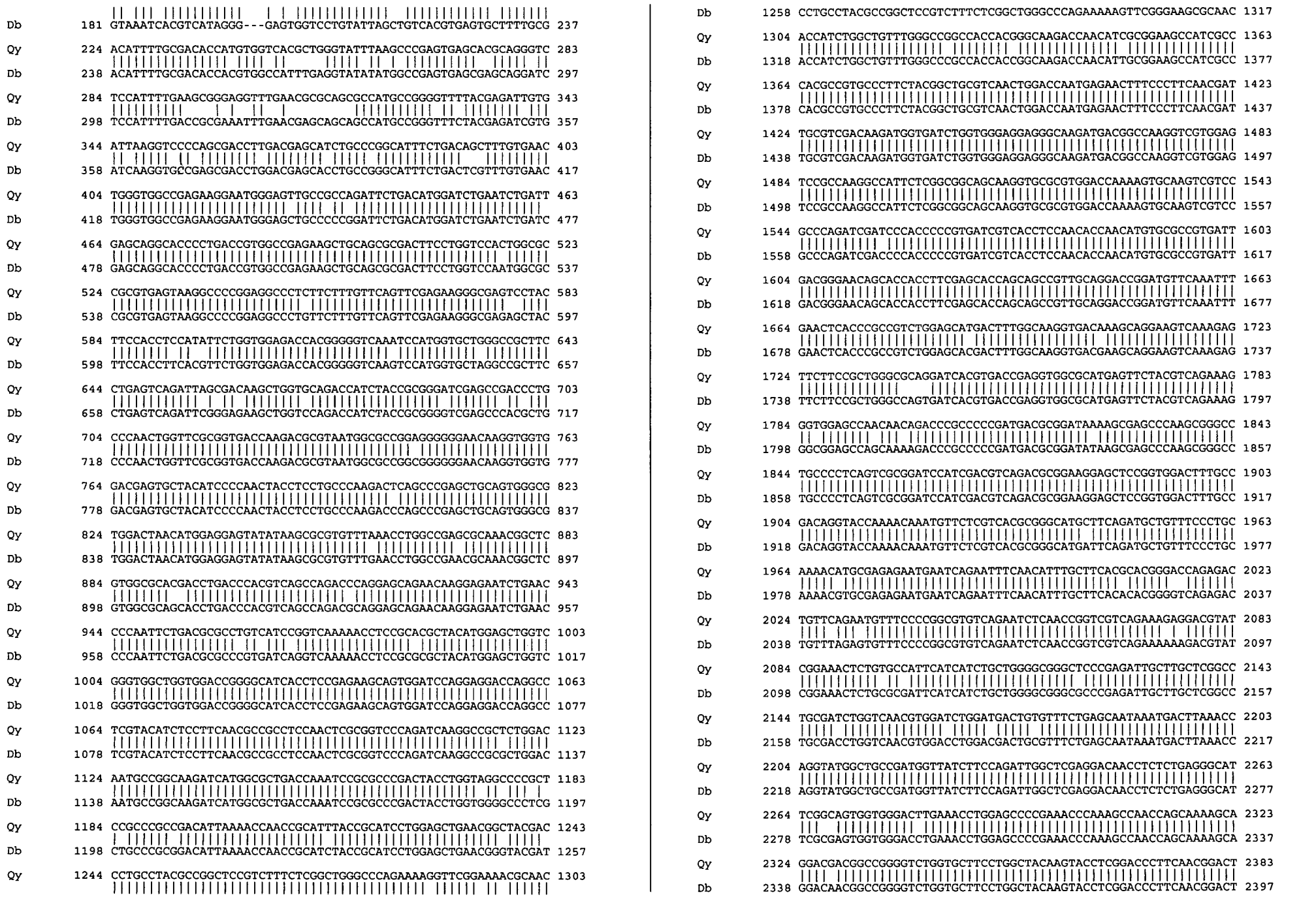

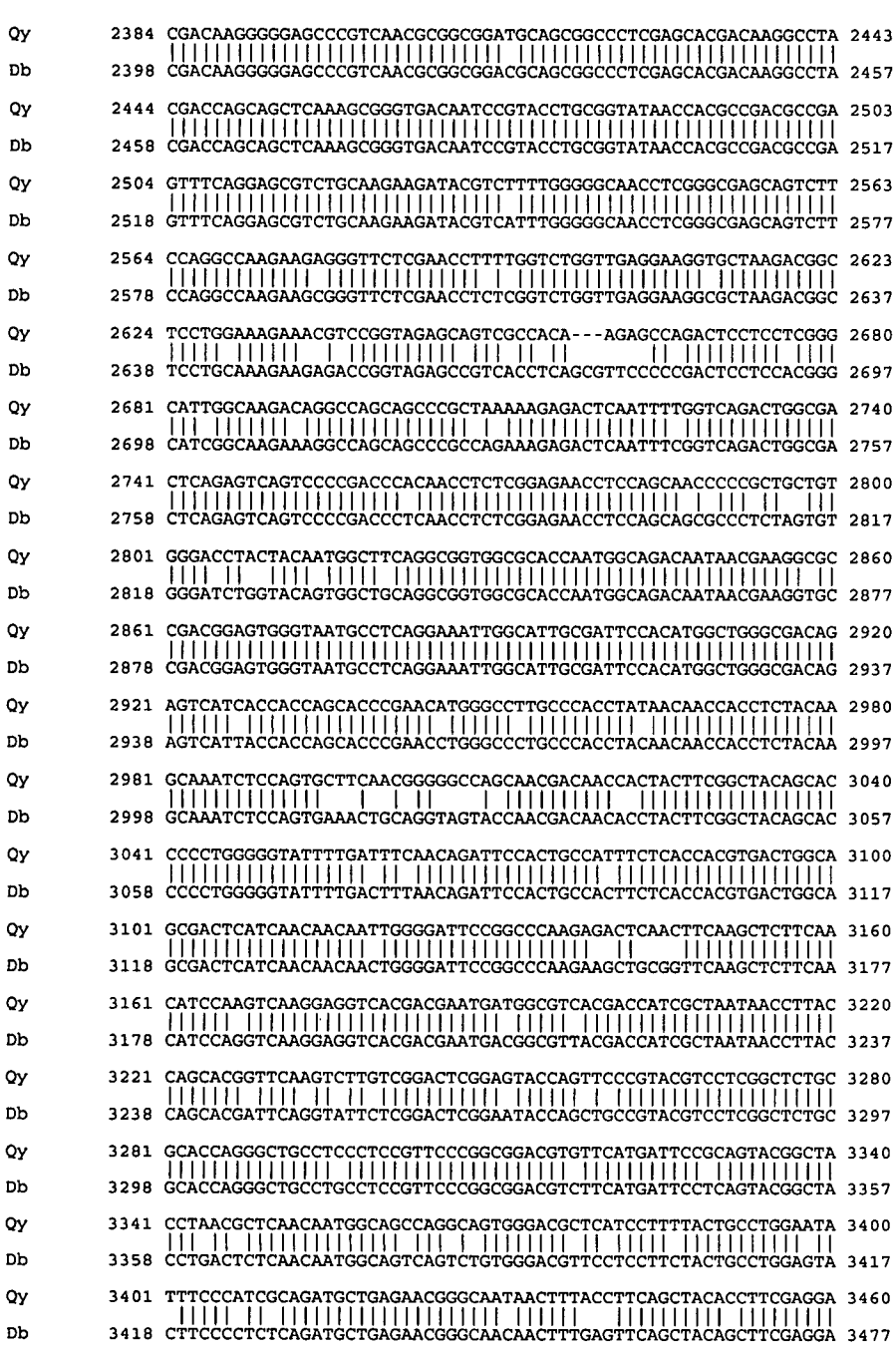
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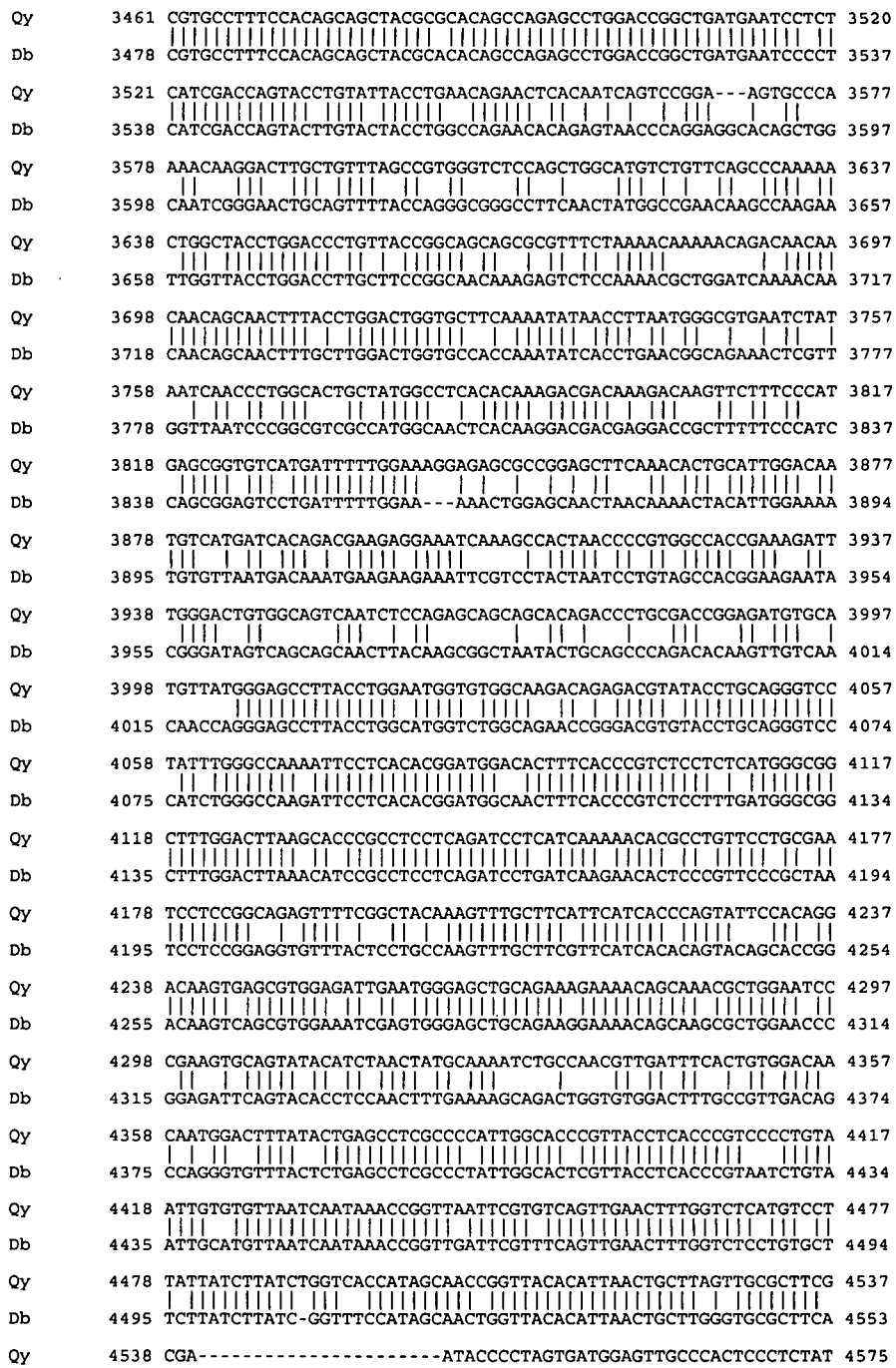
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RESULT 11
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DEFINITION  Adeno-associated virus 7 nonstructural protein and capsid protein
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ACCESSION   AF513851
VERSION     AF513851.1  GI:22652859
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  ORGANISM  Adeno-associated virus - 7
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  AUTHORS   Gao,G.P., Alvira,M.R., Wang,L., Calcedo,R., Johnston,J. and
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  TITLE     Novel adeno-associated viruses from rhesus monkeys as vectors for
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (18), 11854-11859 (2002)
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  AUTHORS   Alvira,M.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-MAY-2002) Institute for Human Gene Therapy,
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ORIGIN

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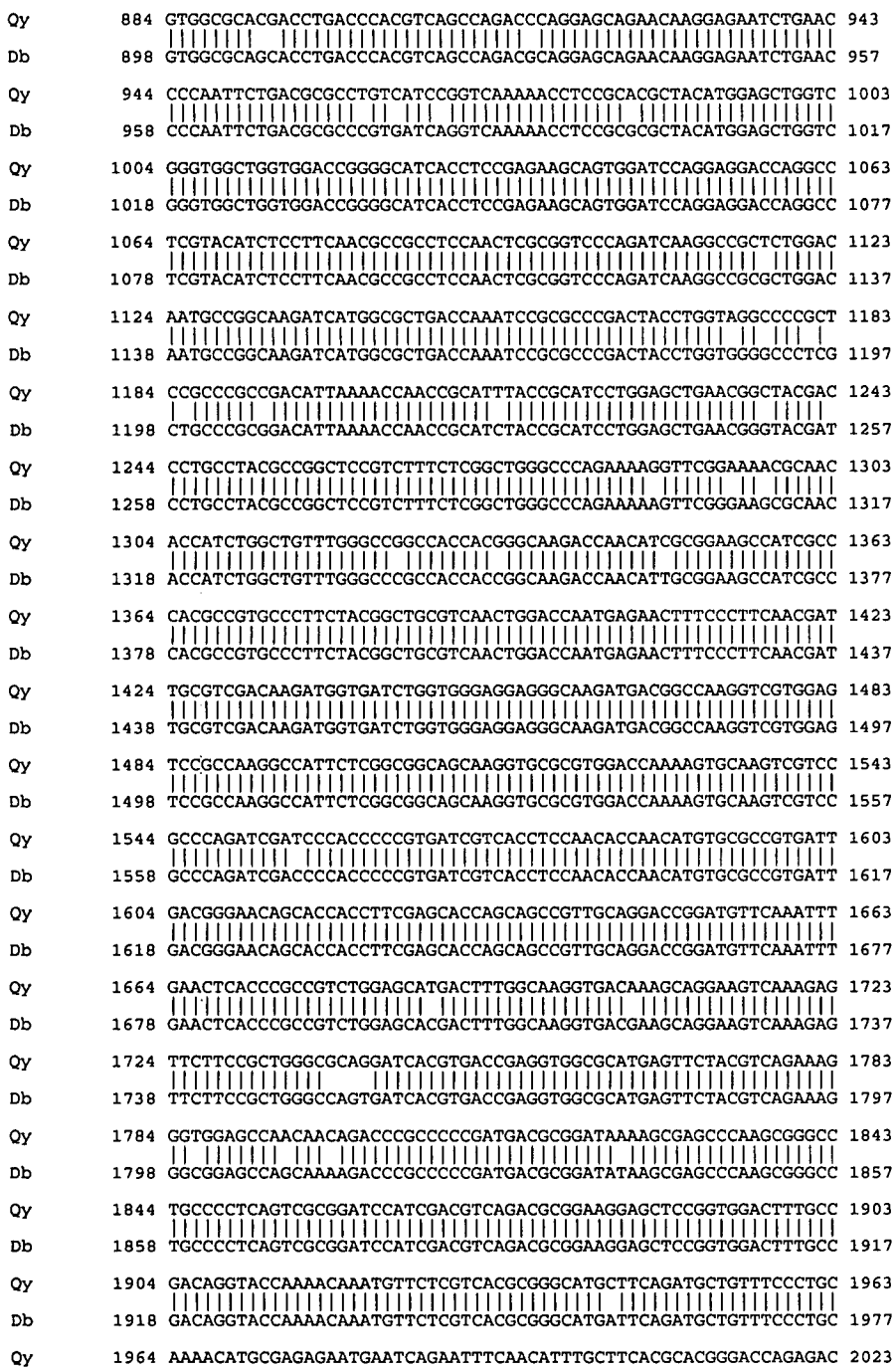
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Qy 2624 TCCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACA---AGAGCCAGACTCCTCCTCGGG 2680
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Db 2938 AGTCATTACCACCAGCACCCGAACCTGGGCCCTGCCCACCTACAACAACCACCTCTACAA 2997
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RESULT 12
AX753250
LOCUS AX753250 4385 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 5 from Patent EP1310571.
ACCESSION AX753250
VERSION AX753250.1 GI:32166107
KEYWORDS .
SOURCE Adeno-associated virus 9
ORGANISM Adeno-associated virus 9
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus;
unclassified Dependovirus.
REFERENCE 1
AUTHORS Gao,G., Wilson,J.M. and Alvira,M.
TITLE A method of detecting and/or identifying adeno-associated virus
(AVV) sequences and isolating novel sequences identified thereby
JOURNAL Patent: EP 1310571-A 5 14-MAY-2003;
The Trustees of The University of Pennsylvania (US)
FEATURES Location/Qualifiers
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ORIGIN

Query Match 72.7%; Score 3404.6; DB 2; Length 4385;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 3782; Conservative 0; Mismatches 527; Indels 13; Gaps 5;

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Qy        216 G-TTTTGCGACATTTTGCGACACCATGTGGTCACGCTGGGTATTTAAGCCCGAGTGAGCA 274

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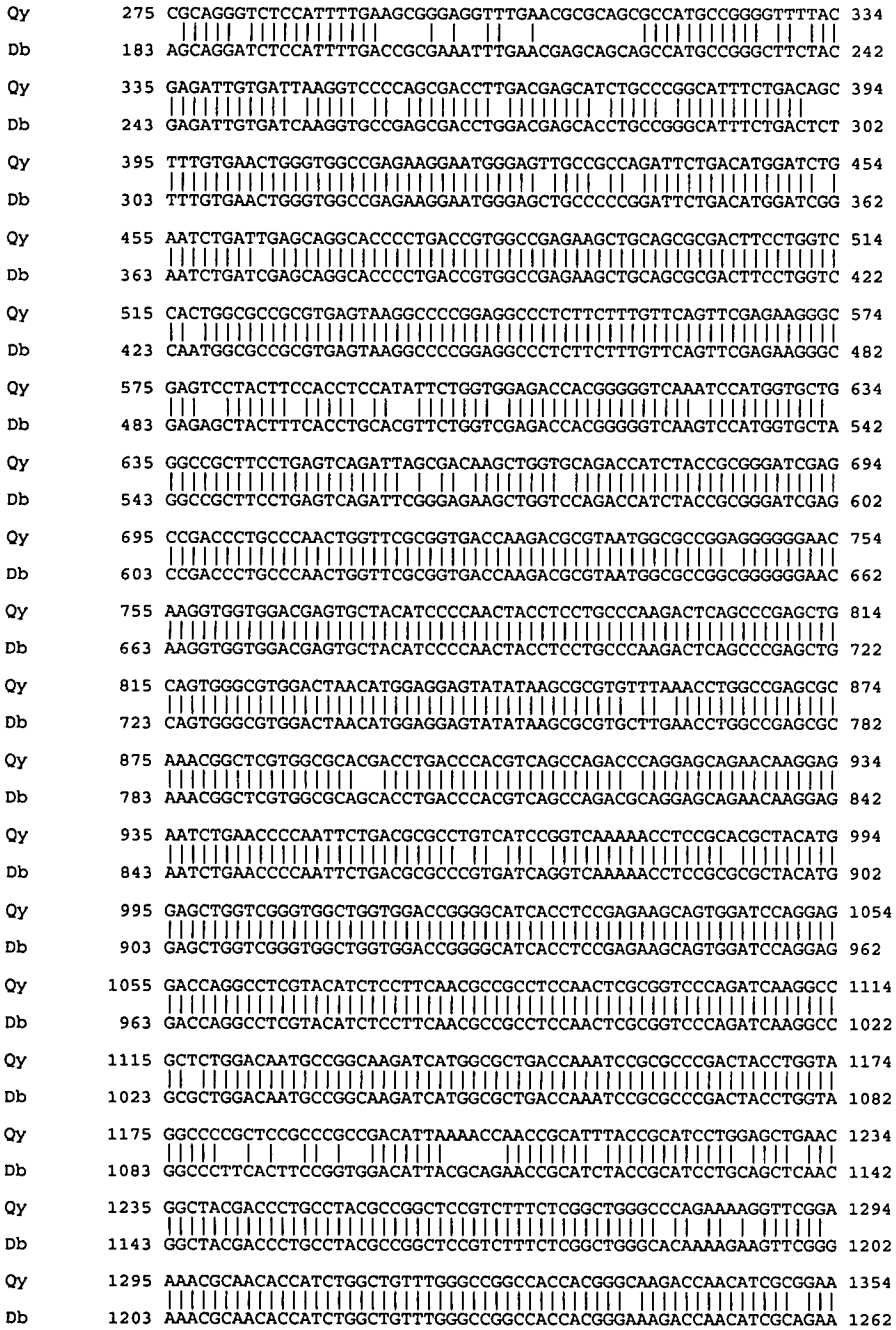

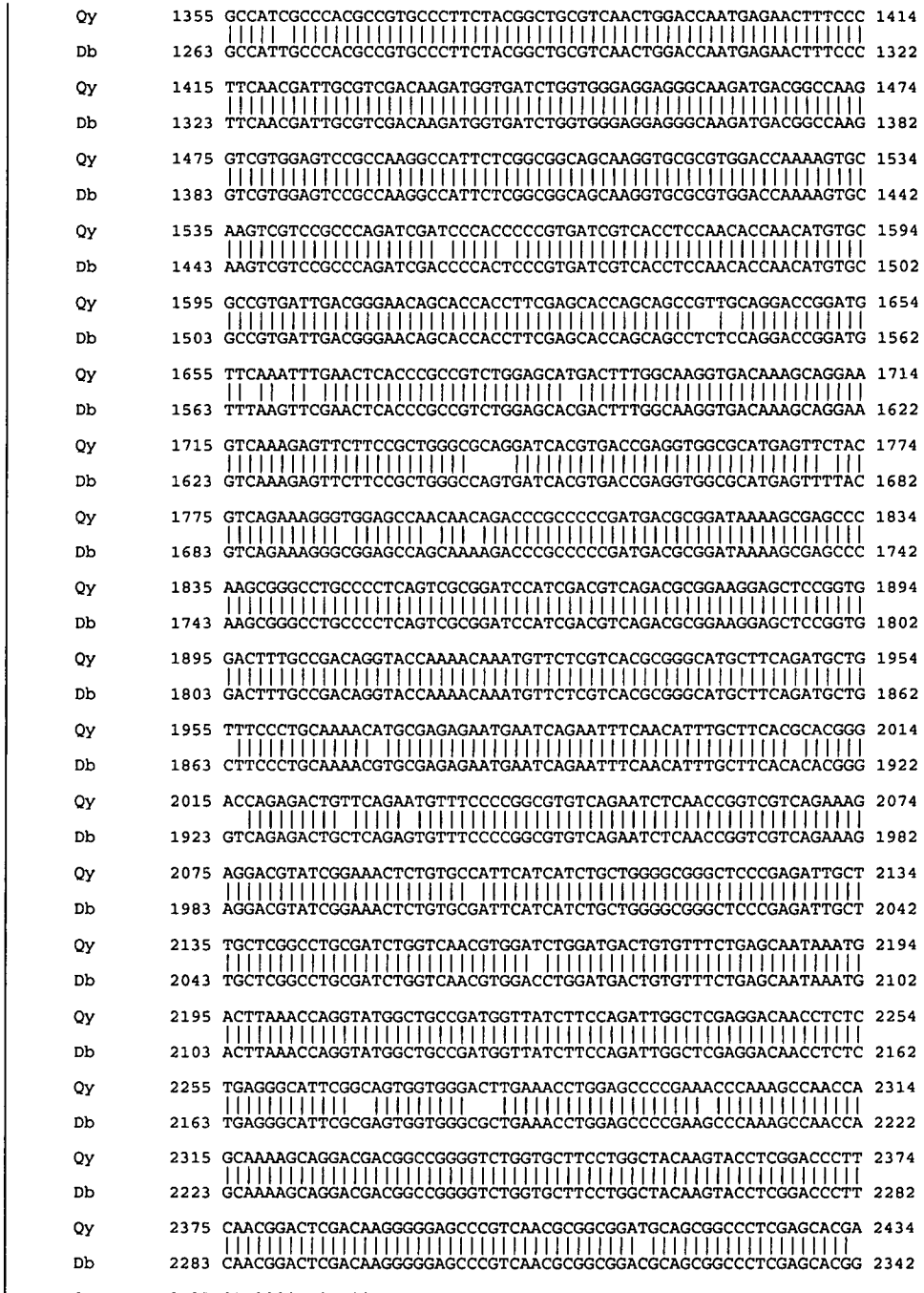

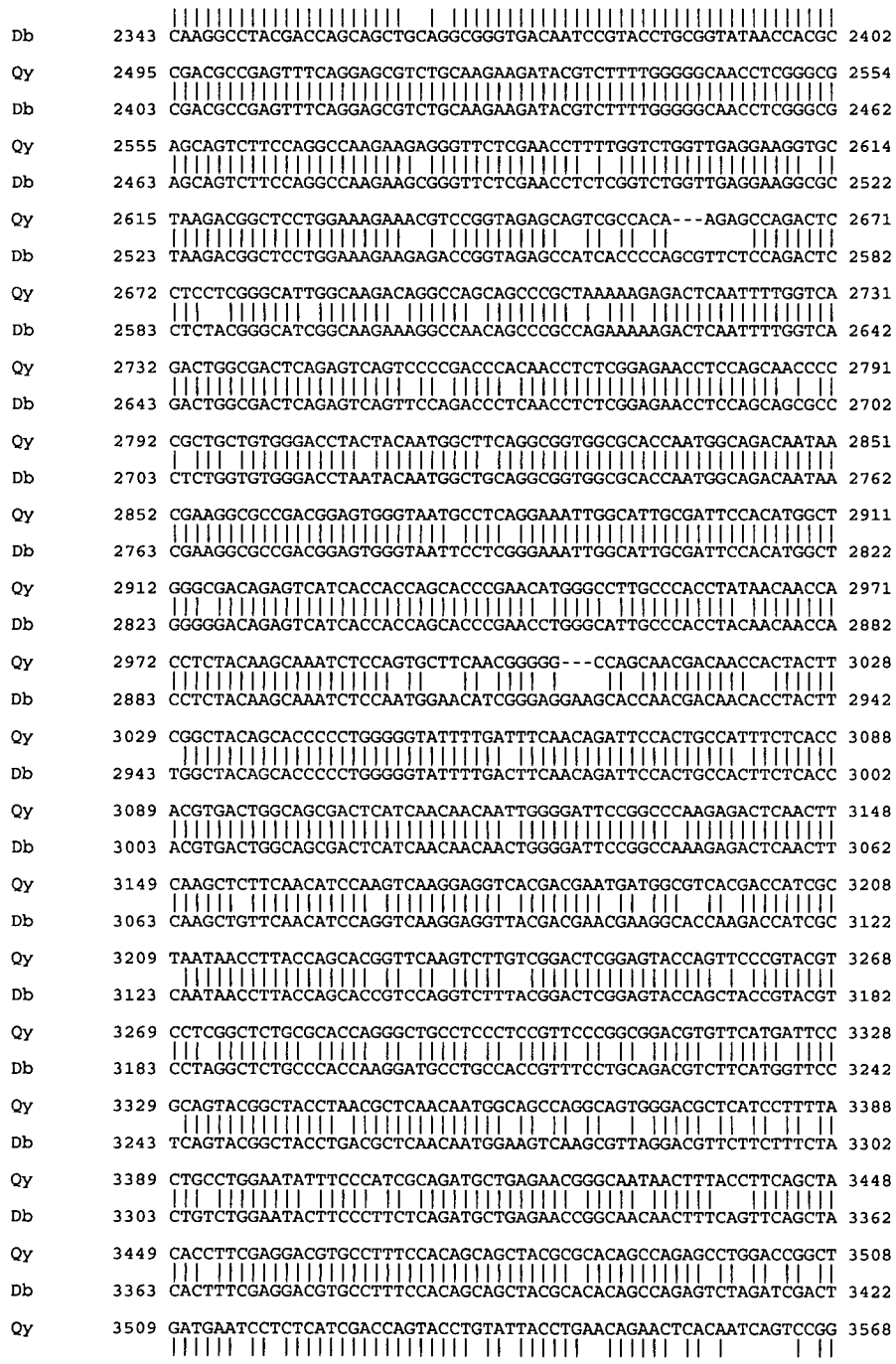

RESULT 13
CQ972063
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DEFINITION Sequence 8 from Patent WO2004108922.
ACCESSION CQ972063
VERSION CQ972063.1 GI:57163376

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KEYWORDS    .
SOURCE      Adeno-associated virus
  ORGANISM  Adeno-associated virus
            Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus;
            unclassified Dependovirus.
REFERENCE   1
  AUTHORS   Rader,D.J. and Wilson,J.M.
  TITLE     Methods and compositions for lowering total cholesterol levels and
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  JOURNAL   Patent: WO 2004108922-A 8 16-DEC-2004;
            The Trustees of The University of Pennsylvania (US)
FEATURES             Location/Qualifiers
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ORIGIN

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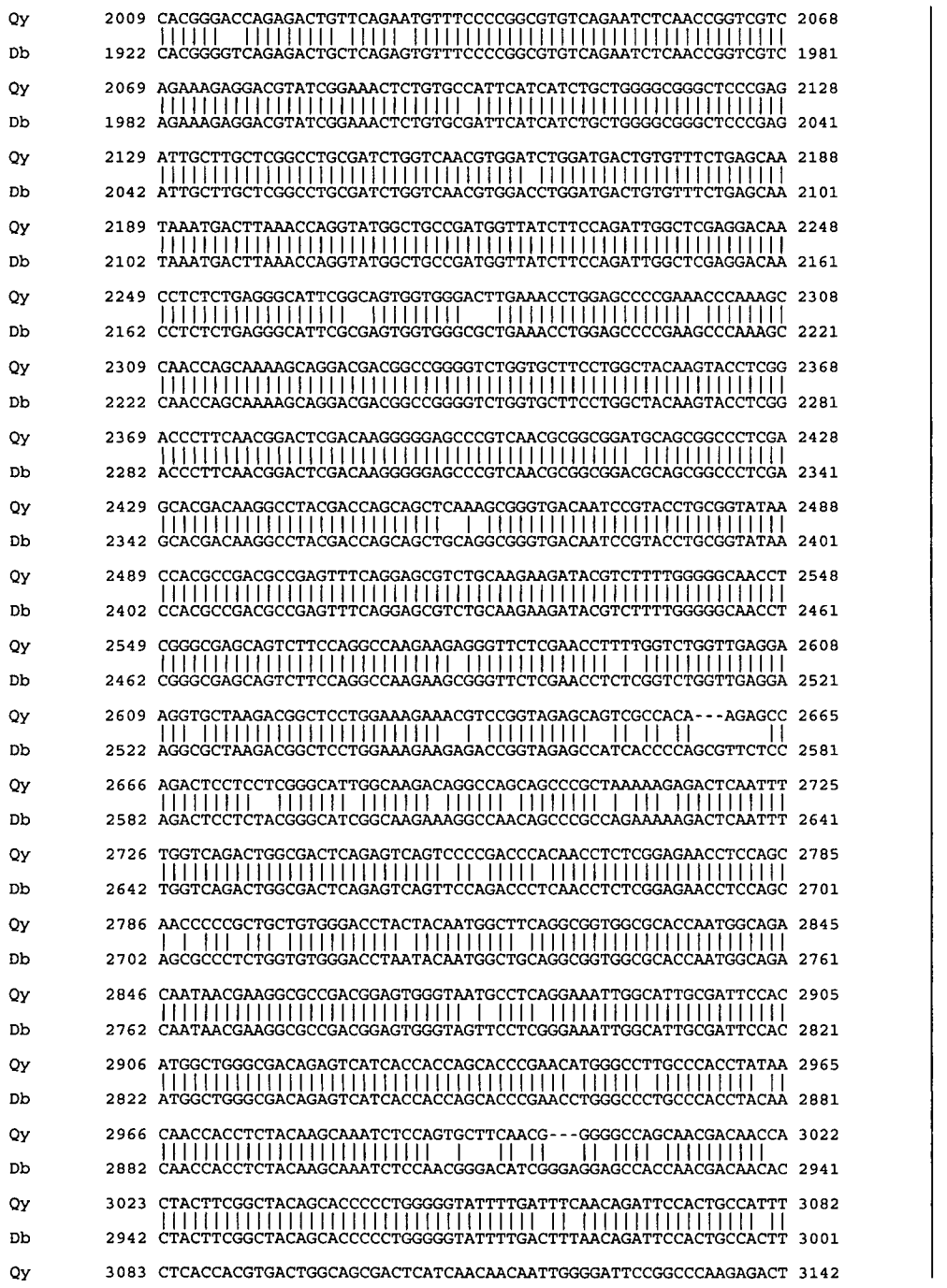
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Qy 2846 CAATAACGAAGGCGCCGACGGAGTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCCAC 2905
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RESULT 14
CS073594
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DEFINITION  Sequence 182 from Patent WO2005033321.
ACCESSION   CS073594
VERSION     CS073594.1  GI:63090490
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Wilson,J.M., Gao,G., Alvira,M.R. and Vandenberghe,L.H.
  TITLE     Adeno-associated virus (aav) clades, sequences, vectors containing
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  JOURNAL   Patent: WO 2005033321-A 182 14-APR-2005;
            The Trustees of the University of Pennsylvania (US)
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ORIGIN

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Db        122 GCTTTTGCGGCATTTTGCGACACCACGTGGCCATTTGAGGTATATATGGCCGAGTGAGCG 181

Qy        275 CGCAGGGTCTCCATTTTGAAGCGGGAGGTTTGAACGCGCAGCGCCATGCCGGGGTTTTAC 334

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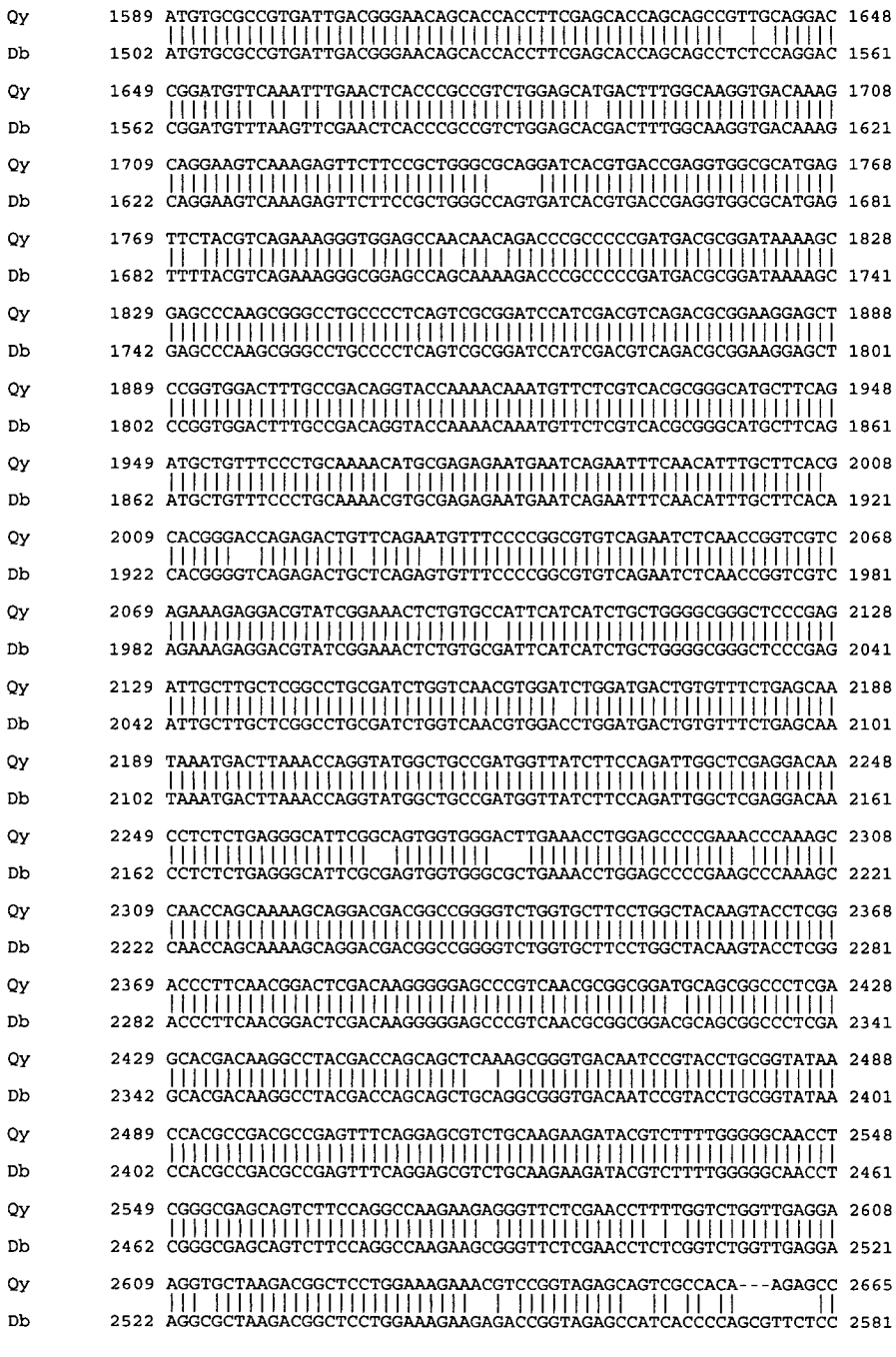
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RESULT 15
AX753249
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DEFINITION  Sequence 4 from Patent EP1310571.
ACCESSION   AX753249
VERSION     AX753249.1  GI:32166106
KEYWORDS    .
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REFERENCE   1
  AUTHORS   Gao,G., Wilson,J.M. and Alvira,M.
  TITLE     A method of detecting and/or identifying adeno-associated virus
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ORIGIN

  Query Match           72.0%;  Score 3370.4;  DB 2;  Length 4393;
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Db        362 AATCTGATCGAGCAGGCACCCCTGACCGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTC 421

Qy        515 CACTGGCGCCGCGTGAGTAAGGCCCCGGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGC 574

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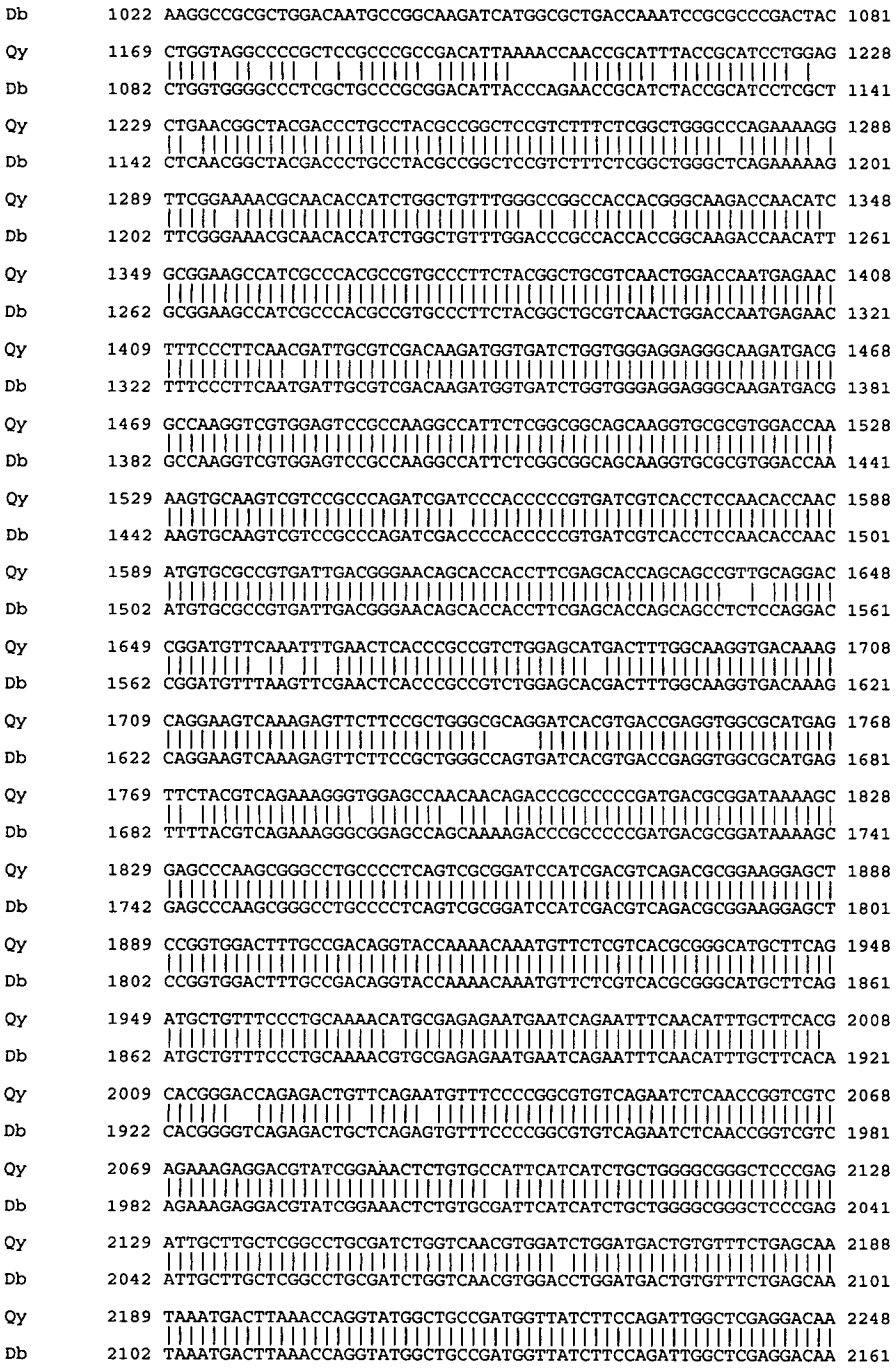
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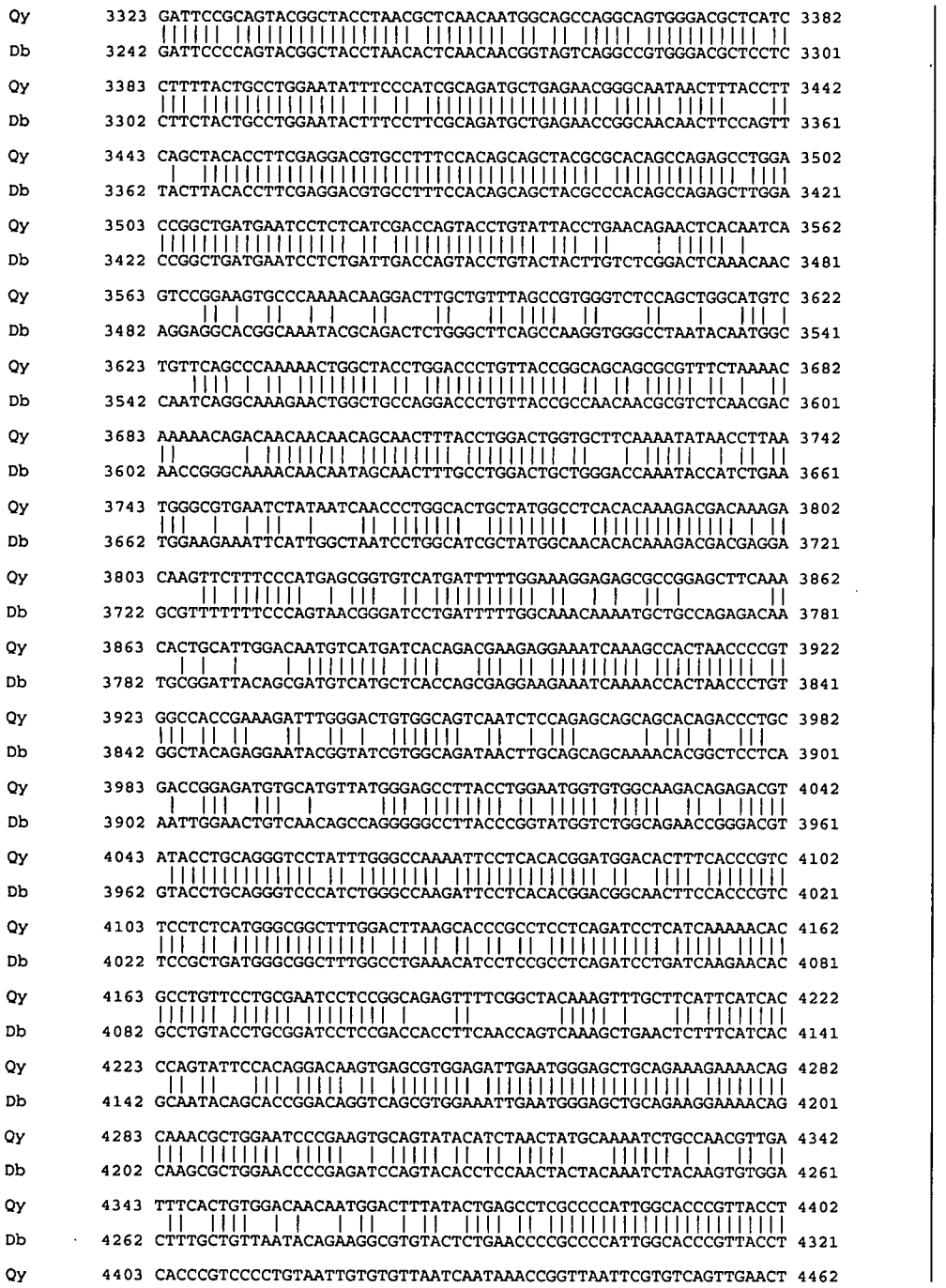

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GenCore version 5.1.9
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Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	128.4	2.7	195	8	CO888893	CO888893 BovGen_17
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c 4	105.2	2.2	969	14	DU710793	DU710793 aav01_fp0
c 5	102.4	2.2	917	14	DU710478	DU710478 aav01_fp0
c 6	102.4	2.2	1165	14	DU710876	DU710876 aav01_fp0
c 7	102.2	2.2	900	14	DU710553	DU710553 aav01_fp0
c 8	101.6	2.2	835	14	DU710062	DU710062 aav01_fp0
c 9	101.4	2.2	894	14	DU710660	DU710660 aav01_fp0
c 10	101.2	2.2	895	14	DU709924	DU709924 aav01_fp0
c 11	100.8	2.2	896	14	DU709985	DU709985 aav01_fp0
c 12	100.6	2.1	919	14	DU710573	DU710573 aav01_fp0
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c 14	100.4	2.1	937	14	DU710803	DU710803 aav01_fp0
c 15	100.4	2.1	943	14	DU710346	DU710346 aav01_fp0
c 16	100.2	2.1	920	14	DU710527	DU710527 aav01_fp0
c 17	99.8	2.1	1032	14	DU710321	DU710321 aav01_fp0
c 18	99.8	2.1	1051	14	DU710319	DU710319 aav01_fp0
c 19	99.8	2.1	1057	14	DU710692	DU710692 aav01_fp0
c 20	99.6	2.1	911	14	DU710661	DU710661 aav01_fp0
c 21	99.4	2.1	882	14	DU710048	DU710048 aav01_fp0
c 22	99.4	2.1	895	14	DU710511	DU710511 aav01_fp0
c 23	99.4	2.1	916	14	DU710467	DU710467 aav01_fp0
c 24	99.4	2.1	946	14	DU710802	DU710802 aav01_fp0
c 25	99.4	2.1	961	14	DU710790	DU710790 aav01_fp0
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c 33	98.6	2.1	922	14	DU710448	DU710448 aav01_fp0
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ALIGNMENTS

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ACCESSION CO892248
VERSION CO892248.1 GI:51822548
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 264)
AUTHORS Hennig,S., Janitz,M., Herwig,R. and Williams,J.
TITLE Generation, annotation, evolutionary analysis and database integration of 14969 cattle EST clusters
JOURNAL Unpublished (2004)
COMMENT Contact: Hennig S
laboraty 123, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
Email: hennig@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting (ONFP) to reduce sequencing redundancy. According to the ONFP procedure, clones that display the same hybridisation matrix with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per ONFP cluster was selected for sequencing. cDNA clones and filters are distributed via Deutsches Ressourcenzentrum fuer Genomforschung GmbH (http://www.rzpd.de).
PCR Primers
FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP) 5'-seq
BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP) 3'-seq
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                     Site_2: SalI; Random primed and directionally cloned in
                     pSport1 vector using NotI
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                     TCGACCCACGCGTCCG-3' adapters (Gibco BRL)"
ORIGIN

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RESULT 2
CO888893/c
LOCUS       CO888893                 195 bp    mRNA    linear   EST 01-SEP-2004
DEFINITION  BovGen_17218 normal cattle brain Bos taurus cDNA clone
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ACCESSION   CO888893
VERSION     CO888893.1  GI:51819178
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 195)
  AUTHORS   Hennig,S., Janitz,M., Herwig,R. and Williams,J.
  TITLE     Generation, annotation, evolutionary analysis and database
            integration of 14969 cattle EST clusters
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Hennig S
            laboraty 123, dept.Lehrach
            Max-Planck-Institut fuer Molekulare Genetik
            Ihnestr.63-73, D-14195 Berlin, Germany
            Tel: +49 30 8413 1612
            Fax: +49 30 8413 1380
            Email: hennig@molgen.mpg.de
            The library was characterised by oligonucleotide fingerprinting
            (ONFP) to reduce sequencing redundancy. According to the ONFP
            procedure, clones that display the same hybridisation matrix with a
            battery of 200 8mer oligonucleotides are grouped into clusters. One
            clone per ONFP cluster was selected for sequencing. cDNA clones and
            filters are distributed via Deutsches Ressourcenzentrum fuer
            Genomforschung GmbH (http://www.rzpd.de).
            PCR PRimers
            FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP) 5'-seq
            BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP) 3'-seq
            Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' (M13RSP).
FEATURES             Location/Qualifiers
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                     /clone_lib="normal cattle brain"
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                     (5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC (T)15-3' and SalI 5'-
                     TCGACCCACGCGTCCG-3' adapters (Gibco BRL)"
ORIGIN

  Query Match             2.7%;  Score 128.4;  DB 8;  Length 195;
  Best Local Similarity   78.9%;  Pred. No. 5.9e-23;
  Matches  153;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy       4224 CAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAATGGGAGCTGCAGAAAGAAAACAGC 4283
             ||||| ||||| ||||| || |||||||||| || |||||| ||||||| | |||||||
Db        194 CAGTACTCCACGGGACAGGTCAGCGTGGAGATCGAGTGGGAGTTGCAGAAGGTAAACAGC 135

Qy       4284 AAACGCTGGAATCCCGAAGTGCAGTATACATCTAACTATGCAAAATCTGCCAACGTTGAT 4343
             ||||| |||||||||||| | ||||| || || |||||     || ||||  || || |||
Db        134 AAACGGTGGAATCCCGAAATTCAGTACACTTCCAACTACAACAAGTCTGTTAATGTGGAT 75

Qy       4344 TTCACTGTGGACAACAATGGACTTTATACTGAGCCTCGCCCCATTGGCACCCGTTACCTC 4403
             || | ||||||||  |||||  | ||| | |||||||||||||||||||| | |||||
Db          74 TTTAATGTGGACATTAATGGCGTGTATTCAGAGCCTCGCCCCATTGGCACCAGATACCTG 15

Qy       4404 ACCCGTCCCCTGTA 4417
             || |||    ||||
Db          14 ACTCGTAATGTGTA 1


RESULT 3
DU710412/c
LOCUS       DU710412                 913 bp    DNA     linear   GSS 15-NOV-2005
DEFINITION  aav01_fp010q008y1 Adeno-Associated Virus Vector Integration
            Junctions Homo sapiens genomic clone aav01_fp010q008, genomic
            survey sequence.
ACCESSION   DU710412
VERSION     DU710412.1  GI:82414138
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 913)
  AUTHORS   Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
            Russell,D.W.
  TITLE     Large-scale Analysis of Adeno-Associated Virus Vector Integration
            Sites
  JOURNAL   Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT     Contact: Miller, D.G.
            Department of Pediatrics
            University of Washington
            HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
            USA
            Tel: 206 685 3882
            Fax: 206 221 5132
            Email: dgmiller@u.washington.edu
            AAV Vector:Chromosome Junction Sequences rescued as plasmids in
            bacteria. Files with names differing only by x1 or y1 contain
            sequence reads from either end of the same AAV provirus. 'y1'
            indicates the 'left' and 'x1' indicates the 'right' primer was used
            to initiate sequencing reactions.
            Seq primer: left, 5'-GATAAGCTGTCAAACATGAGAATTC
            Class: viral tagged.
FEATURES             Location/Qualifiers
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     source          1. .913
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="aav01_fp010q008"
                     /sex="male"
                     /cell_type="Human Primary Fibroblasts"
                     /cell_line="GM05387, Coriell Institute for Medical
                     Research, Camden, NJ"
                     /clone_lib="Adeno-Associated Virus Vector Integration
                     Junctions"
                     /note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction
                     Sequences rescued as plasmids in bacteria. Files with
                     names differing only by x1 or y1 contain sequence reads
                     from either end of the same AAV vector provirus. 'y1'
                     indicates the 'left' and 'x1' indicates the 'right' primer
                     was used to initiate sequencing reactions."
ORIGIN

  Query Match             2.3%;  Score 106.6;  DB 14;  Length 913;
  Best Local Similarity   96.5%;  Pred. No. 8e-17;
  Matches  109;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         35 CTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGA 94
              ||  || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 CTTTGGTCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGA 111

Qy         95 GCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTGG 147
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        110 GCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTTG 58


RESULT 4
DU710793/c
LOCUS       DU710793                969 bp    DNA     linear   GSS 15-NOV-2005
DEFINITION  aav01_fp014q065x1 Adeno-Associated Virus Vector Integration
            Junctions Homo sapiens genomic clone aav01_fp014q065, genomic
            survey sequence.
ACCESSION   DU710793
VERSION     DU710793.1  GI:82414519
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 969)
  AUTHORS   Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
            Russell,D.W.
  TITLE     Large-scale Analysis of Adeno-Associated Virus Vector Integration
            Sites
  JOURNAL   Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT     Contact: Miller, D.G.
            Department of Pediatrics
            University of Washington
            HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
            USA
            Tel: 206 685 3882
            Fax: 206 221 5132
            Email: dgmiller@u.washington.edu
            AAV Vector:Chromosome Junction Sequences rescued as plasmids in
            bacteria. Files with names differing only by x1 or y1 contain
            sequence reads from either end of the same AAV provirus. 'y1'
            indicates the 'left' and 'x1' indicates the 'right' primer was used
            to initiate sequencing reactions.
            Seq primer: right, 5'-ATCACGAGGCCCTTTCGTCTTCAAG
            Class: viral tagged.
FEATURES             Location/Qualifiers
     source          1. .969
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="aav01_fp014q065"
                     /sex="male"
                     /cell_type="Human Primary Fibroblasts"
                     /cell_line="GM05387, Coriell Institute for Medical
                     Research, Camden, NJ"
                     /clone_lib="Adeno-Associated Virus Vector Integration
                     Junctions"
                     /note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction
                     Sequences rescued as plasmids in bacteria. Files with
                     names differing only by x1 or y1 contain sequence reads
                     from either end of the same AAV vector provirus. 'y1'
                     indicates the 'left' and 'x1' indicates the 'right' primer
                     was used to initiate sequencing reactions."
ORIGIN

  Query Match             2.2%;  Score 105.2;  DB 14;  Length 969;
  Best Local Similarity   93.2%;  Pred. No. 2e-16;
  Matches  110;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         30 GCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTC 89
              |||  |  ||| ||  ||||||||||||||||||||||||||||||||||||||||||||
Db        178 GCTTCCAAAGGTCGCCCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTC 119

Qy         90 AGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTGG 147
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        118 AGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTTG 61


RESULT 5
DU710478/c
LOCUS       DU710478                917 bp    DNA     linear   GSS 15-NOV-2005
DEFINITION  aav01_fp010q068y1 Adeno-Associated Virus Vector Integration
            Junctions Homo sapiens genomic clone aav01_fp010q068, genomic
            survey sequence.
ACCESSION   DU710478
VERSION     DU710478.1  GI:82414204
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 917)
  AUTHORS   Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
            Russell,D.W.
  TITLE     Large-scale Analysis of Adeno-Associated Virus Vector Integration
            Sites
  JOURNAL   Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT     Contact: Miller, D.G.
            Department of Pediatrics
            University of Washington
            HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
            USA
            Tel: 206 685 3882
            Fax: 206 221 5132
            Email: dgmiller@u.washington.edu
            AAV Vector:Chromosome Junction Sequences rescued as plasmids in
            bacteria. Files with names differing only by x1 or y1 contain
            sequence reads from either end of the same AAV provirus. 'y1'
            indicates the 'left' and 'x1' indicates the 'right' primer was used
            to initiate sequencing reactions.
            Seq primer: left, 5'-GATAAGCTGTCAAACATGAGAATTC
            Class: viral tagged.
FEATURES             Location/Qualifiers
     source          1. .917
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="aav01_fp010q068"
                     /sex="male"
                     /cell_type="Human Primary Fibroblasts"
                     /cell_line="GM05387, Coriell Institute for Medical
                     Research, Camden, NJ"
                     /clone_lib="Adeno-Associated Virus Vector Integration
```

Junctions"
/note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by x1 or y1 contain sequence reads from either end of the same AAV vector provirus. 'y1' indicates the 'left' and 'x1' indicates the 'right' primer was used to initiate sequencing reactions."
ORIGIN

Query Match 2.2%; Score 102.4; DB 14; Length 917;
Best Local Similarity 90.8%; Pred. No. 1.1e-15;
Matches 109; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy          28 TCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCC 87
               | ||||| |   |   ||  ||||||||||||||||||||||||||||||||||||||
Db         176 TTGCTCAATCTCGGGTGGTTACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCC 117

Qy          88 TCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTGG 147
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db         116 TCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTTG 57
```

RESULT 6
DU710876/c
LOCUS DU710876 1165 bp DNA linear GSS 15-NOV-2005
DEFINITION aav01_fp017q002y1 Adeno-Associated Virus Vector Integration Junctions Homo sapiens genomic clone aav01_fp017q002, genomic survey sequence.
ACCESSION DU710876
VERSION DU710876.1 GI:82414602
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1165)
AUTHORS Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and Russell,D.W.
TITLE Large-scale Analysis of Adeno-Associated Virus Vector Integration Sites
JOURNAL Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT Contact: Miller, D.G.
Department of Pediatrics
University of Washington
HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195, USA
Tel: 206 685 3882
Fax: 206 221 5132
Email: dgmiller@u.washington.edu
AAV Vector:Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by x1 or y1 contain sequence reads from either end of the same AAV provirus. 'y1' indicates the 'left' and 'x1' indicates the 'right' primer was used to initiate sequencing reactions.
Seq primer: left, 5'-GATAAGCTGTCAAACATGAGAATTC
Class: viral tagged.
FEATURES Location/Qualifiers
source 1. .1165
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="aav01_fp017q002"
/sex="male"
/cell_type="Human Primary Fibroblasts"
/cell_line="GM05387, Coriell Institute for Medical Research, Camden, NJ"
/clone_lib="Adeno-Associated Virus Vector Integration Junctions"
/note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by x1 or y1 contain sequence reads from either end of the same AAV vector provirus. 'y1' indicates the 'left' and 'x1' indicates the 'right' primer was used to initiate sequencing reactions."
ORIGIN

Query Match 2.2%; Score 102.4; DB 14; Length 1165;
Best Local Similarity 90.8%; Pred. No. 1.2e-15;
Matches 109; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy          28 TCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCC 87
               || | |||| |      | ||||||||||||||||||||||||||||||||||||||||
Db         226 TCACCCACTAACTTGCTGAGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCC 167

Qy          88 TCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTGG 147
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db         166 TCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTTG 107
```

RESULT 7
DU710553/c
LOCUS DU710553 900 bp DNA linear GSS 15-NOV-2005
DEFINITION aav01_fp011q043y1 Adeno-Associated Virus Vector Integration Junctions Homo sapiens genomic clone aav01_fp011q043, genomic survey sequence.
ACCESSION DU710553
VERSION DU710553.1 GI:82414279
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 900)
AUTHORS Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and Russell,D.W.
TITLE Large-scale Analysis of Adeno-Associated Virus Vector Integration Sites
JOURNAL Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT Contact: Miller, D.G.
Department of Pediatrics
University of Washington
HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195, USA
Tel: 206 685 3882
Fax: 206 221 5132
Email: dgmiller@u.washington.edu
AAV Vector:Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by x1 or y1 contain sequence reads from either end of the same AAV provirus. 'y1' indicates the 'left' and 'x1' indicates the 'right' primer was used to initiate sequencing reactions.
Seq primer: left, 5'-GATAAGCTGTCAAACATGAGAATTC
Class: viral tagged.
FEATURES Location/Qualifiers
source 1. .900
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="aav01_fp011q043"
/sex="male"
/cell_type="Human Primary Fibroblasts"
/cell_line="GM05387, Coriell Institute for Medical Research, Camden, NJ"
/clone_lib="Adeno-Associated Virus Vector Integration Junctions"
/note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction Sequences rescued as plasmids in bacteria. Files with names differing only by x1 or y1 contain sequence reads from either end of the same AAV vector provirus. 'y1' indicates the 'left' and 'x1' indicates the 'right' primer was used to initiate sequencing reactions."
ORIGIN

Query Match 2.2%; Score 102.2; DB 14; Length 900;

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  Best Local Similarity   97.2%;  Pred. No. 1.3e-15;
  Matches  104;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          41 CCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGC 100
               | ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         163 CTGGGGGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGC 104

Qy         101 GAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTGG 147
               ||||||||||||||||||||||||||||||||||||||||||||| |
Db         103 GAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTTG 57


RESULT 8
DU710062/c
LOCUS       DU710062                 835 bp    DNA     linear   GSS 15-NOV-2005
DEFINITION  aav01_fp004q051x1 Adeno-Associated Virus Vector Integration
            Junctions Homo sapiens genomic clone aav01_fp004q051, genomic
            survey sequence.
ACCESSION   DU710062
VERSION     DU710062.1  GI:82413788
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 835)
  AUTHORS   Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
            Russell,D.W.
  TITLE     Large-scale Analysis of Adeno-Associated Virus Vector Integration
            Sites
  JOURNAL   Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT     Contact: Miller, D.G.
            Department of Pediatrics
            University of Washington
            HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
            USA
            Tel: 206 685 3882
            Fax: 206 221 5132
            Email: dgmiller@u.washington.edu
            AAV Vector:Chromosome Junction Sequences rescued as plasmids in
            bacteria. Files with names differing only by x1 or y1 contain
            sequence reads from either end of the same AAV provirus. 'y1'
            indicates the 'left' and 'x1' indicates the 'right' primer was used
            to initiate sequencing reactions.
            Seq primer: right, 5'-ATCACGAGGCCCTTTCGTCTTCAAG
            Class: viral tagged.
FEATURES             Location/Qualifiers
     source          1. .835
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="aav01_fp004q051"
                     /sex="male"
                     /cell_type="Human Primary Fibroblasts"
                     /cell_line="GM05387, Coriell Institute for Medical
                     Research, Camden, NJ"
                     /clone_lib="Adeno-Associated Virus Vector Integration
                     Junctions"
                     /note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction
                     Sequences rescued as plasmids in bacteria. Files with
                     names differing only by x1 or y1 contain sequence reads
                     from either end of the same AAV vector provirus. 'y1'
                     indicates the 'left' and 'x1' indicates the 'right' primer
                     was used to initiate sequencing reactions."
ORIGIN

  Query Match             2.2%;  Score 101.6;  DB 14;  Length 835;
  Best Local Similarity   82.9%;  Pred. No. 1.8e-15;
  Matches  116;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy           8 CTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCC 67
               | |||   |  | | ||   ||     || ||  | |   ||||||||||||||||||||
```

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Db         151 CCCCCGGCCGTCCCTCTTAATCATGGCCTCAGTTCCGAAAACCAAAGGTCGCCCGACGCC 92

Qy          68 CGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACT 127
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          91 CGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACT 32

Qy         128 CCATCACTAGGGGTTCCTGG 147
               |||||||||||||||||| |
Db          31 CCATCACTAGGGGTTCCTTG 12


RESULT 9
DU710660/c
LOCUS       DU710660                 894 bp    DNA     linear   GSS 15-NOV-2005
DEFINITION  aav01_fp013q006x1 Adeno-Associated Virus Vector Integration
            Junctions Homo sapiens genomic clone aav01_fp013q006, genomic
            survey sequence.
ACCESSION   DU710660
VERSION     DU710660.1  GI:82414386
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 894)
  AUTHORS   Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
            Russell,D.W.
  TITLE     Large-scale Analysis of Adeno-Associated Virus Vector Integration
            Sites
  JOURNAL   Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT     Contact: Miller, D.G.
            Department of Pediatrics
            University of Washington
            HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
            USA
            Tel: 206 685 3882
            Fax: 206 221 5132
            Email: dgmiller@u.washington.edu
            AAV Vector:Chromosome Junction Sequences rescued as plasmids in
            bacteria. Files with names differing only by x1 or y1 contain
            sequence reads from either end of the same AAV provirus. 'y1'
            indicates the 'left' and 'x1' indicates the 'right' primer was used
            to initiate sequencing reactions.
            Seq primer: right, 5'-ATCACGAGGCCCTTTCGTCTTCAAG
            Class: viral tagged.
FEATURES             Location/Qualifiers
     source          1. .894
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="aav01_fp013q006"
                     /sex="male"
                     /cell_type="Human Primary Fibroblasts"
                     /cell_line="GM05387, Coriell Institute for Medical
                     Research, Camden, NJ"
                     /clone_lib="Adeno-Associated Virus Vector Integration
                     Junctions"
                     /note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction
                     Sequences rescued as plasmids in bacteria. Files with
                     names differing only by x1 or y1 contain sequence reads
                     from either end of the same AAV vector provirus. 'y1'
                     indicates the 'left' and 'x1' indicates the 'right' primer
                     was used to initiate sequencing reactions."
ORIGIN

  Query Match             2.2%;  Score 101.4;  DB 14;  Length 894;
  Best Local Similarity   99.0%;  Pred. No. 2.1e-15;
  Matches  102;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          45 GCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGC 104
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         163 GCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGC 104
```

```
Qy        105 GCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTGG 147
              |||||||||||||||||||||||||||||||||||||||| |
Db        103 GCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTTG 61


RESULT 10
DU709924/c
LOCUS       DU709924                 895 bp    DNA     linear   GSS 15-NOV-2005
DEFINITION  aav01_fp003q029y1 Adeno-Associated Virus Vector Integration
            Junctions Homo sapiens genomic clone aav01_fp003q029, genomic
            survey sequence.
ACCESSION   DU709924
VERSION     DU709924.1  GI:82413650
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 895)
  AUTHORS   Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
            Russell,D.W.
  TITLE     Large-scale Analysis of Adeno-Associated Virus Vector Integration
            Sites
  JOURNAL   Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT     Contact: Miller, D.G.
            Department of Pediatrics
            University of Washington
            HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
            USA
            Tel: 206 685 3882
            Fax: 206 221 5132
            Email: dgmiller@u.washington.edu
            AAV Vector:Chromosome Junction Sequences rescued as plasmids in
            bacteria. Files with names differing only by x1 or y1 contain
            sequence reads from either end of the same AAV provirus. 'y1'
            indicates the 'left' and 'x1' indicates the 'right' primer was used
            to initiate sequencing reactions.
            Seq primer: left, 5'-GATAAGCTGTCAAACATGAGAATTC
            Class: viral tagged.
FEATURES             Location/Qualifiers
     source          1. .895
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="aav01_fp003q029"
                     /sex="male"
                     /cell_type="Human Primary Fibroblasts"
                     /cell_line="GM05387, Coriell Institute for Medical
                     Research, Camden, NJ"
                     /clone_lib="Adeno-Associated Virus Vector Integration
                     Junctions"
                     /note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction
                     Sequences rescued as plasmids in bacteria. Files with
                     names differing only by x1 or y1 contain sequence reads
                     from either end of the same AAV vector provirus. 'y1'
                     indicates the 'left' and 'x1' indicates the 'right' primer
                     was used to initiate sequencing reactions."
ORIGIN

  Query Match             2.2%;  Score 101.2;  DB 14;  Length 895;
  Best Local Similarity   93.0%;  Pred. No. 2.3e-15;
  Matches  106;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         34 ACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTG 93
              || | | | |   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 ACGGGGTCTGACAGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTG 111

Qy         94 AGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTGG 147
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        110 AGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTTG 57


RESULT 11
DU709985/c
LOCUS       DU709985                 896 bp    DNA     linear   GSS 15-NOV-2005
DEFINITION  aav01_fp003q079y1 Adeno-Associated Virus Vector Integration
            Junctions Homo sapiens genomic clone aav01_fp003q079, genomic
            survey sequence.
ACCESSION   DU709985
VERSION     DU709985.1  GI:82413711
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 896)
  AUTHORS   Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
            Russell,D.W.
  TITLE     Large-scale Analysis of Adeno-Associated Virus Vector Integration
            Sites
  JOURNAL   Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT     Contact: Miller, D.G.
            Department of Pediatrics
            University of Washington
            HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
            USA
            Tel: 206 685 3882
            Fax: 206 221 5132
            Email: dgmiller@u.washington.edu
            AAV Vector:Chromosome Junction Sequences rescued as plasmids in
            bacteria. Files with names differing only by x1 or y1 contain
            sequence reads from either end of the same AAV provirus. 'y1'
            indicates the 'left' and 'x1' indicates the 'right' primer was used
            to initiate sequencing reactions.
            Seq primer: left, 5'-GATAAGCTGTCAAACATGAGAATTC
            Class: viral tagged.
FEATURES             Location/Qualifiers
     source          1. .896
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="aav01_fp003q079"
                     /sex="male"
                     /cell_type="Human Primary Fibroblasts"
                     /cell_line="GM05387, Coriell Institute for Medical
                     Research, Camden, NJ"
                     /clone_lib="Adeno-Associated Virus Vector Integration
                     Junctions"
                     /note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction
                     Sequences rescued as plasmids in bacteria. Files with
                     names differing only by x1 or y1 contain sequence reads
                     from either end of the same AAV vector provirus. 'y1'
                     indicates the 'left' and 'x1' indicates the 'right' primer
                     was used to initiate sequencing reactions."
ORIGIN

  Query Match             2.2%;  Score 100.8;  DB 14;  Length 896;
  Best Local Similarity   93.8%;  Pred. No. 3e-15;
  Matches  105;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         36 TGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAG 95
              ||||||      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 TGAGGCAAACTTACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAG 111

Qy         96 CGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTGG 147
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        110 CGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTTG 59


RESULT 12
DU710573/c
LOCUS       DU710573                 919 bp    DNA     linear   GSS 15-NOV-2005
DEFINITION  aav01_fp011q064x1 Adeno-Associated Virus Vector Integration
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            Junctions Homo sapiens genomic clone aav01_fp011q064, genomic
            survey sequence.
ACCESSION   DU710573
VERSION     DU710573.1  GI:82414299
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 919)
  AUTHORS   Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
            Russell,D.W.
  TITLE     Large-scale Analysis of Adeno-Associated Virus Vector Integration
            Sites
  JOURNAL   Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT     Contact: Miller, D.G.
            Department of Pediatrics
            University of Washington
            HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
            USA
            Tel: 206 685 3882
            Fax: 206 221 5132
            Email: dgmiller@u.washington.edu
            AAV Vector:Chromosome Junction Sequences rescued as plasmids in
            bacteria. Files with names differing only by x1 or y1 contain
            sequence reads from either end of the same AAV provirus. 'y1'
            indicates the 'left' and 'x1' indicates the 'right' primer was used
            to initiate sequencing reactions.
            Seq primer: right, 5'-ATCACGAGGCCCTTTCGTCTTCAAG
            Class: viral tagged.
FEATURES             Location/Qualifiers
     source          1. .919
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="aav01_fp011q064"
                     /sex="male"
                     /cell_type="Human Primary Fibroblasts"
                     /cell_line="GM05387, Coriell Institute for Medical
                     Research, Camden, NJ"
                     /clone_lib="Adeno-Associated Virus Vector Integration
                     Junctions"
                     /note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction
                     Sequences rescued as plasmids in bacteria. Files with
                     names differing only by x1 or y1 contain sequence reads
                     from either end of the same AAV vector provirus. 'y1'
                     indicates the 'left' and 'x1' indicates the 'right' primer
                     was used to initiate sequencing reactions."
ORIGIN

  Query Match             2.1%;  Score 100.6;  DB 14;  Length 919;
  Best Local Similarity   96.3%;  Pred. No. 3.4e-15;
  Matches  103;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         41 CCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGC 100
              ||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 CCTCCCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGC 108

Qy        101 GAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTGG 147
              |||||||||||||||||||||||||||||||||||||||||||||| |
Db        107 GAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTTG 61


RESULT 13
DU710776/c
LOCUS       DU710776                945 bp    DNA     linear   GSS 15-NOV-2005
DEFINITION  aav01_fp014q045x1 Adeno-Associated Virus Vector Integration
            Junctions Homo sapiens genomic clone aav01_fp014q045, genomic
            survey sequence.
ACCESSION   DU710776
VERSION     DU710776.1  GI:82414502
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 945)
  AUTHORS   Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
            Russell,D.W.
  TITLE     Large-scale Analysis of Adeno-Associated Virus Vector Integration
            Sites
  JOURNAL   Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT     Contact: Miller, D.G.
            Department of Pediatrics
            University of Washington
            HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
            USA
            Tel: 206 685 3882
            Fax: 206 221 5132
            Email: dgmiller@u.washington.edu
            AAV Vector:Chromosome Junction Sequences rescued as plasmids in
            bacteria. Files with names differing only by x1 or y1 contain
            sequence reads from either end of the same AAV provirus. 'y1'
            indicates the 'left' and 'x1' indicates the 'right' primer was used
            to initiate sequencing reactions.
            Seq primer: right, 5'-ATCACGAGGCCCTTTCGTCTTCAAG
            Class: viral tagged.
FEATURES             Location/Qualifiers
     source          1. .945
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="aav01_fp014q045"
                     /sex="male"
                     /cell_type="Human Primary Fibroblasts"
                     /cell_line="GM05387, Coriell Institute for Medical
                     Research, Camden, NJ"
                     /clone_lib="Adeno-Associated Virus Vector Integration
                     Junctions"
                     /note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction
                     Sequences rescued as plasmids in bacteria. Files with
                     names differing only by x1 or y1 contain sequence reads
                     from either end of the same AAV vector provirus. 'y1'
                     indicates the 'left' and 'x1' indicates the 'right' primer
                     was used to initiate sequencing reactions."
ORIGIN

  Query Match             2.1%;  Score 100.6;  DB 14;  Length 945;
  Best Local Similarity   96.3%;  Pred. No. 3.5e-15;
  Matches  103;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         41 CCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGC 100
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 CAGGTCTACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGC 108

Qy        101 GAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTGG 147
              |||||||||||||||||||||||||||||||||||||||||||||| |
Db        107 GAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTTG 61


RESULT 14
DU710803/c
LOCUS       DU710803                937 bp    DNA     linear   GSS 15-NOV-2005
DEFINITION  aav01_fp014q087x1 Adeno-Associated Virus Vector Integration
            Junctions Homo sapiens genomic clone aav01_fp014q087, genomic
            survey sequence.
ACCESSION   DU710803
VERSION     DU710803.1  GI:82414529
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
```

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REFERENCE   1  (bases 1 to 937)
  AUTHORS   Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
            Russell,D.W.
  TITLE     Large-scale Analysis of Adeno-Associated Virus Vector Integration
            Sites
  JOURNAL   Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT     Contact: Miller, D.G.
            Department of Pediatrics
            University of Washington
            HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
            USA
            Tel: 206 685 3882
            Fax: 206 221 5132
            Email: dgmiller@u.washington.edu
            AAV Vector:Chromosome Junction Sequences rescued as plasmids in
            bacteria. Files with names differing only by x1 or y1 contain
            sequence reads from either end of the same AAV provirus. 'y1'
            indicates the 'left' and 'x1' indicates the 'right' primer was used
            to initiate sequencing reactions.
            Seq primer: right, 5'-ATCACGAGGCCCTTTCGTCTTCAAG
            Class: viral tagged.
FEATURES             Location/Qualifiers
     source          1. .937
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="aav01_fp014q087"
                     /sex="male"
                     /cell_type="Human Primary Fibroblasts"
                     /cell_line="GM05387, Coriell Institute for Medical
                     Research, Camden, NJ"
                     /clone_lib="Adeno-Associated Virus Vector Integration
                     Junctions"
                     /note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction
                     Sequences rescued as plasmids in bacteria. Files with
                     names differing only by x1 or y1 contain sequence reads
                     from either end of the same AAV vector provirus. 'y1'
                     indicates the 'left' and 'x1' indicates the 'right' primer
                     was used to initiate sequencing reactions."
ORIGIN

  Query Match             2.1%;  Score 100.4;  DB 14;  Length 937;
  Best Local Similarity   90.7%;  Pred. No. 3.9e-15;
  Matches  107;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          30 GCTCACTGAGGCCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTC 89
               ||   ||  ||   || | ||||||||||||||||||||||||||||||||||||||||||
Db         178 GCAGCCTTGGGGTCGGAGCCCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTC 119

Qy          90 AGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTGG 147
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db         118 AGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTTG 61


RESULT 15
DU710346/c
LOCUS       DU710346               943 bp    DNA     linear   GSS 15-NOV-2005
DEFINITION  aav01_fp008q066y1 Adeno-Associated Virus Vector Integration
            Junctions Homo sapiens genomic clone aav01_fp008q066, genomic
            survey sequence.
ACCESSION   DU710346
VERSION     DU710346.1  GI:82414072
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 943)
  AUTHORS   Miller,D.G., Trobridge,G.D., Petek,L.M., Jacobs,M.A., Kaul,R. and
            Russell,D.W.
  TITLE     Large-scale Analysis of Adeno-Associated Virus Vector Integration
            Sites
  JOURNAL   Journal of Virology 79 (17), 11434-11442 (2005)
COMMENT     Contact: Miller, D.G.
            Department of Pediatrics
            University of Washington
            HSB RR349A, Box 356320, 1959 NE Pacific Street, Seattle, WA 98195,
            USA
            Tel: 206 685 3882
            Fax: 206 221 5132
            Email: dgmiller@u.washington.edu
            AAV Vector:Chromosome Junction Sequences rescued as plasmids in
            bacteria. Files with names differing only by x1 or y1 contain
            sequence reads from either end of the same AAV provirus. 'y1'
            indicates the 'left' and 'x1' indicates the 'right' primer was used
            to initiate sequencing reactions.
            Seq primer: left, 5'-GATAAGCTGTCAAACATGAGAATTC
            Class: viral tagged.
FEATURES             Location/Qualifiers
     source          1. .943
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="aav01_fp008q066"
                     /sex="male"
                     /cell_type="Human Primary Fibroblasts"
                     /cell_line="GM05387, Coriell Institute for Medical
                     Research, Camden, NJ"
                     /clone_lib="Adeno-Associated Virus Vector Integration
                     Junctions"
                     /note="Vector: AAV2-TOA; AAV Vector:Chromosome Junction
                     Sequences rescued as plasmids in bacteria. Files with
                     names differing only by x1 or y1 contain sequence reads
                     from either end of the same AAV vector provirus. 'y1'
                     indicates the 'left' and 'x1' indicates the 'right' primer
                     was used to initiate sequencing reactions."
ORIGIN

  Query Match             2.1%;  Score 100.4;  DB 14;  Length 943;
  Best Local Similarity   99.0%;  Pred. No. 3.9e-15;
  Matches  101;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          46 CGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCG 105
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         158 CGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCG 99

Qy         106 CGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTGG 147
               |||||||||||||||||||||||||||||||||||||||| |
Db          98 CGCAGAGAGGGAGTGGCCAACTCCATCACTAGGGGTTCCTTG 57


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Job time : 20433 secs
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